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OM nucleic - nucleic search, using sw model

Run on: August 2, 2005, 17:23:41 ; Search time 187.176 Seconds  
(without alignments)  
5979.480 Million cell updates/sec

Title: US-09-830-144-1\_COPY\_408\_1091

Perfect score: 684  
Sequence: 1 gtagagcttcgcgcagttatc.....cattacagttatcttgcag 684

Scoring table:  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	684	100.0	1788	3	US-09-529-279-14
2	684	100.0	1788	4	US-10-158-895-14
3	684	100.0	2656	2	US-08-685-625A-5
4	684	100.0	2656	3	US-09-529-279-3
5	684	100.0	2656	4	US-10-158-895-3
6	684	100.0	2769	4	US-09-949-016-4031
7	585.4	85.6	2443	2	US-08-685-625A-1
8	141.2	20.6	76264	4	US-09-949-016-15773
9	104	15.2	507	4	US-09-270-767-106
10	104	15.2	507	4	US-09-270-767-15388
11	72	10.5	601	4	US-09-949-016-142616
12	54.6	8.0	426	4	US-09-513-999C-3587
13	54.6	8.0	1365	3	US-09-221-235-6
14	54.6	8.0	1365	3	US-09-221-928-6
15	54.6	8.0	1365	3	US-09-221-527-6
16	54.6	8.0	1365	3	US-09-221-236-6
17	54.6	8.0	1365	3	US-09-221-416-6
18	54.6	8.0	1365	3	US-09-221-245-6
19	54.6	8.0	1365	3	US-09-163-115-6
20	54.6	8.0	1365	3	US-09-221-528-6
21	54.6	8.0	1365	3	US-09-593-553-6
22	54.6	8.0	1365	3	US-09-221-237-6
23	54.6	8.0	1365	3	US-09-757-982-6
24	54.6	8.0	2119	4	US-09-399-588-1
25	54.6	8.0	2120	3	US-09-221-235-4
26	54.6	8.0	2120	3	US-09-221-928-4
27	54.6	8.0	2120	3	US-09-221-527-4

28	54.6	8.0	2120	3	US-09-221-236-4	Sequence 4, Appli
29	54.6	8.0	2120	3	US-09-221-416-4	Sequence 4, Appli
30	54.6	8.0	2120	3	US-09-221-245-4	Sequence 4, Appli
31	54.6	8.0	2120	3	US-09-163-115-4	Sequence 4, Appli
32	54.6	8.0	2120	3	US-09-221-528-4	Sequence 4, Appli
33	54.6	8.0	2120	3	US-09-593-553-4	Sequence 4, Appli
34	54.6	8.0	2120	3	US-09-221-237-4	Sequence 4, Appli
35	54.6	8.0	2120	4	US-09-757-982-4	Sequence 4, Appli
36	52	7.6	1251	2	US-09-340-930-2	Sequence 2, Appli
37	52	7.6	1251	3	US-09-468-442-2	Sequence 2, Appli
38	52	7.6	1353	2	US-09-211-930-8	Sequence 8, Appli
39	52	7.6	1353	3	US-09-340-993-8	Sequence 8, Appli
40	52	7.6	1353	4	US-09-468-442-8	Sequence 8, Appli
41	52	7.6	1542	3	US-09-345-473B-13	Sequence 13, Appli
42	52	7.6	3201	2	US-09-211-930-1	Sequence 1, Appli
43	52	7.6	3201	3	US-09-340-993-1	Sequence 1, Appli
44	52	7.6	3201	3	US-09-468-442-1	Sequence 1, Appli
45	52	7.6	3201	3	US-09-468-442-1	Sequence 1, Appli

## ALIGNMENTS

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RESULT 1
US-09-529-279-14
; Sequence 14, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIOHKO
; APPLICANT: TSUCHIYA, MAYAYUKI
; TITLE OR INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529, 279
; PRIOR APPLICATION NUMBER: 2000-04-11
; PRIOR FILING DATE: 1998-10-22
; PRIOR FILING DATE: 1997-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(1776)
US-09-529-279-14
Query Match 100.0%; Score 684; DB 3; Length 1788;
Best local Similarity 100.0%; Pred. No. 1.1e-217;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTAGAGCTTGGCGAGTATCCGCTGTAACCATCTAATATGTAAGCTTATGAGCC 60
232 GTAGAGCTTGGCGAGTATCCGCTGTAACCATCTAATATGTAAGCTTATGAGCC 291
61 TGTGTAATCAGTGTGCTGTGATGTAATGTAATGTAAGGAGGCTTTATATATG 120
292 TGTGTAATCAGTGTGCTGTGATGTAATGTAATGTAAGGAGGCTTTATATATG 351
121 CTGATGATGCTGAACCATTCCTATATATGCTGCTCCACGCAATGATGCTGTTA 180
352 CTGATGATGCTGAACCATTCCTATATATGCTGCTCCACGCAATGATGCTGTTA 411
181 CAGGTTCCAGAGAGTGGCTTATCTTACAGATGCAACCAAGGCTTATTCACAGG 240
412 CAGGTTCCAGAGAGTGGCTTATCTTACAGATGCAACCAAGGCTTATTCACAGG 471
241 GACCTGAACCAACCACTTACTGCTGTTGACAGGAGGAGACGTTCTAAATTTGAT 300
472 GACCTGAACCAACCACTTACTGCTGTTGACAGGAGGAGACGTTCTAAATTTGAT 531
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QY 301 TTGGTACAGCCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTCTGCTGG 360  
Db 532 TTGGTACAGCCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTCTGCTGG 591  
QY 361 ATGGCAGCTGAAGTTTGAAGGTGATTAACAGTGAATAATGAGAGTCTTCAGCTGG 420  
Db 592 ATGGCAGCTGAAGTTTGAAGGTGATTAACAGTGAATAATGAGAGTCTTCAGCTGG 651  
QY 421 GGTATTAATCTTTGGAGAGTGAACGCGTGGAAACCTTGATGATGAGTGGGCCCA 480  
Db 652 GGTATTAATCTTTGGAGAGTGAACGCGTGGAAACCTTGATGATGAGTGGGCCCA 711  
QY 481 GCTTTCCGAATCATGATGGGCTGTTCAATATGTAATCTGACACCACTGATTAATAATTA 540  
Db 712 GCTTTCCGAATCATGATGGGCTGTTCAATATGTAATCTGACACCACTGATTAATAATTA 771  
QY 541 CCTAAGCCCATTTGAGAGCCTGATGACTGTTGTTGCTTAAGATCCCTCCAGCGCCT 600  
Db 772 CCTAAGCCCATTTGAGAGCCTGATGACTGTTGTTGCTTAAGATCCCTCCAGCGCCT 831  
QY 601 TCAATGAGGAAATTTGTAATAATTAATGACTCACTTGATGCGGTACTTTCCAGAGCAGAT 660  
Db 832 TCAATGAGGAAATTTGTAATAATTAATGACTCACTTGATGCGGTACTTTCCAGAGCAGAT 891  
QY 661 GAGCCATTACAGTATCCTTGTGAG 684  
Db 892 GAGCCATTACAGTATCCTTGTGAG 915

## RESULT 2

US-10-158-895-14  
; Sequence 14, Application US/10158895  
; Patent No. 6551840  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHIMIRO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/10/158, 895  
; PRIOR FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: US/09/529, 279  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: JP 9/290188  
; PRIOR FILING DATE: 1997-10-22  
; NUMBER OF SEQ. ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ. ID NO 14  
; LENGTH: 1788  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (7)..(1776)  
US-10-158-895-14

Query Match 100.0%; Score 684; DB 4; Length 1788;  
Best Local Similarity 100.0%; Pred. No. 1.1e-217;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGAGCTTGGGAGTTATCCGTGTGAACCAATCTTAATATGTAAGCTTATGAGACC 60  
Db 232 GTAGAGCTTGGGAGTTATCCGTGTGAACCAATCTTAATATGTAAGCTTATGAGACC 291  
QY 61 TCGTTGAATCCAGTGTGCTTGTGATGAAATATGCTGAAGGGGGCTCTTATATATATG 120  
Db 292 TCGTTGAATCCAGTGTGCTTGTGATGAAATATGCTGAAGGGGGCTCTTATATATATG 351  
QY 121 CTGCAATGTGTGAACCAATGCTATATTAATGCTGCGCCAGCAATGATGGTGTTA 180

Db 352 CTGCAATGTGTGAACCAATGCTATATTAATGCTGCGCCAGCAATGATGGTGTTA 411  
QY 181 CAGTTTCCCAAGAGTGGTTATCTTCAAGAGTCAACCAAGCGCTAATTCACAG 240  
Db 412 CAGTTTCCCAAGAGTGGTTATCTTCAAGAGTCAACCAAGCGCTAATTCACAG 471  
QY 241 GACCTGAACCAACCAATTAATGCTGCTGTTGCAAGGGGGAGCAGTTCTAATAATTTGTGAT 300  
Db 472 GACCTGAACCAACCAATTAATGCTGCTGTTGCAAGGGGGAGCAGTTCTAATAATTTGTGAT 531  
QY 301 TTGGTACAGCCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTCTGCTGG 360  
Db 532 TTGGTACAGCCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTCTGCTGG 591  
QY 361 ATGGCAGCTGAAGTTTGAAGGTGATTAACAGTGAATAATGAGAGTCTTCAGCTGG 420  
Db 592 ATGGCAGCTGAAGTTTGAAGGTGATTAACAGTGAATAATGAGAGTCTTCAGCTGG 651  
QY 421 GGTATTAATCTTTGGAGAGTGAACGCGTGGAAACCTTGATGATGAGTGGGCCCA 480  
Db 652 GGTATTAATCTTTGGAGAGTGAACGCGTGGAAACCTTGATGATGAGTGGGCCCA 711  
QY 481 GCTTTCCGAATCATGATGGGCTGTTCAATATGTAATCTGACACCACTGATTAATAATTA 540  
Db 712 GCTTTCCGAATCATGATGGGCTGTTCAATATGTAATCTGACACCACTGATTAATAATTA 771  
QY 541 CCTAAGCCCATTTGAGAGCCTGATGACTGTTGTTGCTTAAGATCCCTCCAGCGCCT 600  
Db 772 CCTAAGCCCATTTGAGAGCCTGATGACTGTTGTTGCTTAAGATCCCTCCAGCGCCT 831  
QY 601 TCAATGAGGAAATTTGTAATAATTAATGACTCACTTGATGCGGTACTTTCCAGAGCAGAT 660  
Db 832 TCAATGAGGAAATTTGTAATAATTAATGACTCACTTGATGCGGTACTTTCCAGAGCAGAT 891  
QY 661 GAGCCATTACAGTATCCTTGTGAG 684  
Db 892 GAGCCATTACAGTATCCTTGTGAG 915

## RESULT 3

US-08-685-625A-5  
; Sequence 5, Application US/08685625A  
; Patent No. 5945301  
; GENERAL INFORMATION:  
; APPLICANT: UENO, Naoto  
; APPLICANT: MATSUMOTO, Kunihiko  
; APPLICANT: IRIE, Kenji  
; TITLE OF INVENTION: NOVEL KINASE IN TGF-BETA FAMILY SIGNAL  
; TITLE OF INVENTION: TRANSDUCTION SYSTEM  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685, 625A  
; FILING DATE: 24-JUL-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-253549  
; FILING DATE: 29-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M.  
; REGISTRATION NUMBER: 36, 607  
; REFERENCE/DOCKET NUMBER: 001560-267

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2656 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 183..1922  
US-08-685-625A-5

Query Match 100.0%; Score 684; DB 2; Length 2656;  
Best Local Similarity 100.0%; Pred. No. 1.4e-217;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGAGCTGGGCGAGTATCCCGGTGAACCATCTAATATTGTAAGCTTTATGAGCC 60  
DB 408 GTAGAGCTGGGCGAGTATCCCGGTGAACCATCTAATATTGTAAGCTTTATGAGCC 467  
QY 61 TGTGTAATCCAGTGTCTGTGATGGAATATGCTGAAGGGGCTCTTTATATATG 120  
DB 468 TGTGTAATCCAGTGTCTGTGATGGAATATGCTGAAGGGGCTCTTTATATATG 527  
QY 121 CTGATGCTGTGTAACCATTCATATTATATCTGCTGCCACGCAATGATGTTGTTTA 180  
DB 528 CTGATGCTGTGTAACCATTCATATTATCTGCTGCCACGCAATGATGTTGTTTA 587  
QY 181 CAGGTTCCCAAGAGTGGCTTATCTTCAAGCATGCAACCAAGGCTTAATCAAG 240  
DB 588 CAGGTTCCCAAGAGTGGCTTATCTTCAAGCATGCAACCAAGGCTTAATCAAG 647  
QY 241 GACCTGAACCAACCACTTACTGCTGTTGCAAGGGGCAAGTCTTAAATTTGAT 300  
DB 648 GACCTGAACCAACCACTTACTGCTGTTGCAAGGGGCAAGTCTTAAATTTGAT 707  
QY 301 TTTGTAACGCTGTGACATTCAACACATGACCAATTAACAAGGAGTGTCTGG 360  
DB 708 TTTGTAACGCTGTGACATTCAACACATGACCAATTAACAAGGAGTGTCTGG 767  
QY 361 ATGCACTGAAGTTTGAAGTATTAATCAAGTGAATAATGTAAGTCTTCAAGCTG 420  
DB 768 ATGCACTGAAGTTTGAAGTATTAATCAAGTGAATAATGTAAGTCTTCAAGCTG 827  
QY 421 GGTATTAATCTTTGGGAAGTATACGCGTGGAAACCTTTGATGAGATTGTGGCCA 480  
DB 828 GGTATTAATCTTTGGGAAGTATACGCGTGGAAACCTTTGATGAGATTGTGGCCA 887  
QY 481 GCTTCCGAATCATGTGGGCTGTTCATATGTAATGTAATCTGACCACTGATTAATAATTA 540  
DB 888 GCTTCCGAATCATGTGGGCTGTTCATATGTAATGTAATCTGACCACTGATTAATAATTA 947  
QY 541 CCTAAGCCATTGAGAGCTGTATGACTGTGTTGTTGTTAAAGATCTTCCAGGCGCT 600  
DB 948 CCTAAGCCATTGAGAGCTGTATGACTGTGTTGTTGTTAAAGATCTTCCAGGCGCT 1007  
QY 601 TCAATGAGGAATTTGTAATAATATGACTGACTGATGAGGCTTCTTCCAGAGCAGAT 660  
DB 1008 TCAATGAGGAATTTGTAATAATATGACTGACTGATGAGGCTTCTTCCAGAGCAGAT 1067  
QY 661 GAGCATTACAGTATCTTGTGAG 684  
DB 1068 GAGCATTACAGTATCTTGTGAG 1091

RESULT 4  
US-09-529-279-3  
Sequence 3, Application US/09529279  
Patent No. 6451617  
GENERAL INFORMATION:

APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIRO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES

FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/09/529, 279  
CURRENT FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3

LENGTH: 2656  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (183)..(1919)  
US-09-529-279-3

Query Match 100.0%; Score 684; DB 3; Length 2656;  
Best Local Similarity 100.0%; Pred. No. 1.4e-217;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGAGCTGGGCGAGTATCCCGGTGAACCATCTAATATTGTAAGCTTTATGAGCC 60  
DB 408 GTAGAGCTGGGCGAGTATCCCGGTGAACCATCTAATATTGTAAGCTTTATGAGCC 467  
QY 61 TGTGTAATCCAGTGTCTGTGATGGAATATGCTGAAGGGGCTCTTTATATATG 120  
DB 468 TGTGTAATCCAGTGTCTGTGATGGAATATGCTGAAGGGGCTCTTTATATATG 527  
QY 121 CTGATGCTGTGTAACCATTCATATTATATCTGCTGCCACGCAATGATGTTGTTTA 180  
DB 528 CTGATGCTGTGTAACCATTCATATTATCTGCTGCCACGCAATGATGTTGTTTA 587  
QY 181 CAGGTTCCCAAGAGTGGCTTATCTTCAAGCATGCAACCAAGGCTTAATCAAG 240  
DB 588 CAGGTTCCCAAGAGTGGCTTATCTTCAAGCATGCAACCAAGGCTTAATCAAG 647  
QY 241 GACCTGAACCAACCACTTACTGCTGTTGCAAGGGGCAAGTCTTAAATTTGAT 300  
DB 648 GACCTGAACCAACCACTTACTGCTGTTGCAAGGGGCAAGTCTTAAATTTGAT 707  
QY 301 TTTGTAACGCTGTGACATTCAACACATGACCAATTAACAAGGAGTGTCTGG 360  
DB 708 TTTGTAACGCTGTGACATTCAACACATGACCAATTAACAAGGAGTGTCTGG 767  
QY 361 ATGCACTGAAGTTTGAAGTATTAATCAAGTGAATAATGTAAGTCTTCAAGCTG 420  
DB 768 ATGCACTGAAGTTTGAAGTATTAATCAAGTGAATAATGTAAGTCTTCAAGCTG 827  
QY 421 GGTATTAATCTTTGGGAAGTATACGCGTGGAAACCTTTGATGAGATTGTGGCCA 480  
DB 828 GGTATTAATCTTTGGGAAGTATACGCGTGGAAACCTTTGATGAGATTGTGGCCA 887  
QY 481 GCTTCCGAATCATGTGGGCTGTTCATATGTAATGTAATCTGACCACTGATTAATAATTA 540  
DB 888 GCTTCCGAATCATGTGGGCTGTTCATATGTAATGTAATCTGACCACTGATTAATAATTA 947  
QY 541 CCTAAGCCATTGAGAGCTGTATGACTGTGTTGTTGTTAAAGATCTTCCAGGCGCT 600  
DB 948 CCTAAGCCATTGAGAGCTGTATGACTGTGTTGTTGTTAAAGATCTTCCAGGCGCT 1007  
QY 601 TCAATGAGGAATTTGTAATAATATGACTGACTGATGAGGCTTCTTCCAGAGCAGAT 660  
DB 1008 TCAATGAGGAATTTGTAATAATATGACTGACTGATGAGGCTTCTTCCAGAGCAGAT 1067  
QY 661 GAGCATTACAGTATCTTGTGAG 684  
DB 1068 GAGCATTACAGTATCTTGTGAG 1091

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Query Match      100.0%; Score 684; DB 4; Length 2656;
Best Local Similarity 100.0%; Pred. No. 1.4e-217;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Oy      601 TCAATGAGAAATTTGGAAAATATATATACCTGACTGATGCGGATCTTTCCAGAGCAGAT 660
Db      1008 TCAATGAGAGAAATTTGGAAAATATATATACCTGATGATGCGGATCTTTCCAGAGCAGAT 1067
Oy      661 GAGCCATTACGATACCTTGTCCAG 684
Db      1068 GAGCCATTACGATACCTTGTCCAG 1091

RESULT 6
US-09-949-016-4031
/ Sequence 4031, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: C0001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FaStSeq for Windows Version 4.0
/ SEQ ID NO 4031
/ LENGTH: 2769
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-4031

Query Match      100.0%; Score 684; DB 4; Length 2769;
Best Local Similarity 100.0%; Pred. No. 1,4e-217;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GTAGAGCTTGGCAGCTTATCCCGTGTGAACCATCTCTATTTGTAAGCTTTATGAGCC 60
Db      388 GTAGAGCTTGGCAGCTTATCCCGTGTGAACCATCTCTATTTGTAAGCTTTATGAGCC 447
Oy      61 TGCCTGAATCCAGTGTGCTTTGTGTGATGGAATATGCTGAAGGGGCTCTTTATATATGTG 120
Db      448 TGCCTGAATCCAGTGTGCTTTGTGTGATGGAATATGCTGAAGGGGCTCTTTATATATGTG 507
Oy      121 CTGACATGTGTGTCGAACCAATTCGATATATATCTGTGCGCAGCAAGATAGTGTGTTTA 180
Db      508 CTGACATGTGTGTCGAACCAATTCGATATATATCTGTGCGCAGCAAGATAGTGTGTTTA 567
Oy      181 CAGGTGTTCCCAAGAGTGGCTTATCTTACAGCATGCAACCCAAAGCGCTAATTCACAGG 240
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Oy      241 GACCTGAACCAACCAAACTTATCTCTGAGTTCAGAGGGGGACAGTTCTTAATAAATTTGTGAT 300
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Db      688 TTTTGATACAGCTGTGACATTTACAGACACACATGCAACCAATTAACAAGGGAGTGTGCTTGG 747
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Oy      421 GGTATTAATCTTTGGGAAGTATPACGCGTCGGAAACCCCTTTGATGATGATTTGGTGCCCA 480
Db      808 GGTATTAATCTTTGGGAAGTATPACGCGTCGGAAACCCCTTTGATGATGATTTGGTGCCCA 867
Oy      481 GCTTTCGATTCATGATGGGCTGTTCACTTAATATGATCTGATCACTGATTAATAAATTTTAA 540

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Db 868 GCTTCGAATCATGTGGGCTGTTCAATATGTACTGACACCACTGATATAAATTTA 927  
Qy 541 CCTAAGCCCATTTGAGAGCTTATATGCTGTTGTTGTTAAAGATCCCTCCAGGCGCT 600  
Db 928 CCTAAGCCCATTTGAGAGCTTATATGCTGTTGTTGTTAAAGATCCCTCCAGGCGCT 987  
Qy 601 TCAATGAGGAAATTTGAAATATATGACTCACTTGATGCGGTACTTCCAGAGCAGAT 660  
Db 988 TCAATGAGGAAATTTGAAATATATGACTCACTTGATGCGGTACTTCCAGAGCAGAT 1047  
Qy 661 GAGCCATTACAGTATCCTTGTGAG 684  
Db 1048 GAGCCATTACAGTATCCTTGTGAG 1071

RESULT 7  
US-08-685-625A-1

; Sequence 1, Application US/08685625A  
; Patent No. 5945301  
; GENERAL INFORMATION:  
; APPLICANT: UENO, Naoto  
; APPLICANT: MATSUMOTO, Kunihiko  
; APPLICANT: IRIE, Kenji  
; TITLE OF INVENTION: NOVEL KINASE IN TGF-BETA FAMILY SIGNAL  
; TITLE OF INVENTION: TRANSDUCTION SYSTEM  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685,625A  
; FILING DATE: 24-JUL-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-253549  
; FILING DATE: 29-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuch, Donna M.  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 001560-267  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO. 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2443 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 157..1893  
; US-08-685-625A-1

## Query Match 85.6%; Score 585.4; DB 2; Length 2443;

Best Local Similarity 91.1%; Pred. No. 1.1e-184;  
Matches 622; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 1 GTAGAGCTTCGGACGTTATCCGTTGTAACATCTTAATATGTAAGCTTTATGAGCC 60  
Db 382 GTAGAGCTTCGGACGTTATCCGTTGTAACATCTTAATATGTAAGCTTTATGAGCC 441

Qy 61 TGCTTAATCAAGTGTGTCTTGTGATGATATCTGTAAGGGGGCTTTATATATATGTG 120  
Db 442 TGCTTAATCAAGTGTGTCTTGTGATGATATCTGTAAGGGGGCTTTATATATATGTG 501  
Qy 121 CTGATATGCTGTGAACATATGATATATATATATATATATATATATATATATATAT 180  
Db 502 CTGATATGCTGTGAACATATGATATATATATATATATATATATATATATATATAT 561  
Qy 181 CAGTGTCCCAAGGAGTGTGCTTATCTTCAAGCATGCAACCAAGGCTTAATTCACAGG 240  
Db 562 CAGTGTCCCAAGGAGTGTGCTTATCTTCAAGCATGCAACCAAGGCTTAATTCACAGG 621  
Qy 241 GACCTGAACCAACCACTTACTGCTGTGTCAGGGGGGACGTTCTTAATAATTTGTAT 300  
Db 622 GACCTGAACCTCCAACTTCTGCTGTGTCAGGGGGGACGTTCTTAATAATTTGTAT 681  
Qy 301 TTGCTACAGCTGTGATTCATTCACACATGACATATACCAAGGGGAGTGTGCTTG 360  
Db 682 TTGCTACAGCTGTGATTCATTCACACATGACATATATTAAGGGGAGTGTGCTTG 741  
Qy 361 ATGGACCTGAAGTTTGAAGTATATATATATATATATATATATATATATATATAT 420  
Db 742 ATGGACCTGAAGTTTGAAGTATATATATATATATATATATATATATATATATAT 801  
Qy 421 GGTATTAATCTTGTGGAGTATACGGCTGCGAAACCTTTGATGATGATGTGGCCCA 480  
Db 802 GGTATTAATCTTGTGGAGTATATACGGCTGCGAAACCTTTGATGATGATGTGGCCCA 861  
Qy 481 GCTTTCGAATCATGTGGGCTGTTCAATATATGATCTGACACCACTGATATAAATTTA 540  
Db 862 GCTTTCGAATCATGTGGGCTGTTCAATATATGATCTGACACCACTGATATAAATTTA 921  
Qy 541 CCTAAGCCCATTTGAGAGCTTATATGATCTGTTGTTGTTAAAGATCCCTCCAGGCGCT 600  
Db 922 CCTAAGCCCATTTGAGAGCTTATATGACGCTGTGTGTTAAAGATCCCTCCAGGCGCT 981  
Qy 601 TCAATGAGGAAATTTGAAATATATGACTCACTTGATGCGGTACTTCCAGAGCAGAT 660  
Db 982 TCAATGAGGAAATTTGAAATATATGACTCACTTGATGCGGTACTTCCAGAGCAGAT 1041  
Qy 661 GAGCCATTACAGTATCCTTGTGCA 683  
Db 1042 GAGCCATTACAGTATCCTTGTGCA 1064

## RESULT 8

; US-09-949-016-15773  
; Sequence 15773, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: C1601307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15773  
; LENGTH: 76264  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(76264)  
; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-15773

Query Match	20.6%;	Score 141.2;	DB 4;	Length 76264
Best Local Similarity	97.9%;	Pred. No. 1.8e-35;		
Matches 143;	Conservative	0;	Mismatches 3;	Indels 0;

QY	118	GTGCTGCACTGGTGTGTCGAAACCATTTGCGCATATATATCTGCTGCGCCACCGAATGAAGTGTGT	177
Db	28834	GTGCTGCACTGGTGTGTCGAAACCATTTGCGCATATATATCTGCTGCGCCACCGAATGAAGTGTGT	28893
OY	178	TTTACAGTTCGCCAAGAGTGGCTTAATCTTCAACAGCTGCATGCCAAAGCGCTAATTTCAC	237
Db	28894	TTTACAGTTCGCCAAGAGTGGCTTAATCTTCAACAGCTGCATGCCAAAGCGCTAATTTCAC	28953
OY	238	AGGGAACCTGAAACCAACCAACTTACT	263
Db	28954	AGGGAACCTGAAACCAACCAAGTAACT	28979

RESULT 9  
US-09-27

Sequence 106, Application US/09270767  
 Patent No. 6703491  
 GENERAL INFORMATION:  
 APPLICANT: Homburger et al.  
 TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
 FILE REFERENCE: File Reference: 7326-094  
 CURRENT APPLICATION NUMBER: US/09/270,767  
 CURRENT FILING DATE: 1999-03-17  
 NUMBER OF SEQ ID NOS: 62517  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 106  
 LENGTH: 507  
 TYPE: DNA  
 ORGANISM: *Drosophila melanogaster*  
 US-09-270-767-106

Query Match	15.2%	Score 104;	DB 4;	Length 507;
Best Local Similarity	58.9%	Pred. No. 2.9e-24;		
Matches 198; Conservative	0;	Mismatches 135;	Indels 3;	Gaps 1;

QY	346	GGGAGTCTCTGGANATGGCACTGAAGTTTTGAAAGTAAGTAATTAATTAACGTGAAAATGT	405
Db	501	GGATTGCCCCTTGATGAGTGCGCCCGAGGCTCTTGAAAGGCTCCAAAGTAATACGAAAAGGT	444
QY	406	GACGCTCTTCACTGGGGATTAATTCTTTGGGAAGTAAACGCGTCGGAAAACCTTTGAT	465
Db	441	GACATTTTCAGCTGGGCCCAATTGTTCTATGGGAGGTTCTGTCCAGGAACGACCCTTTAA	382
QY	466	GAGATGGTGGGCCACCTTTCGAAATCANTGGGGCTGTCCTAAATGTAATCTGCACACA	523
Db	381	GGCAT---CGACAAATCTTACACATCTCCAGTGGAAAATTTCAAGAGGTAAAGGCCCGCG	325
QY	526	CTGATAAAAAATTTACCTTAAGCCCATTTGAGACCTGATGACTCGTTGTTGGTCTTAAAGAT	585
Db	324	CTGCTACACATTCGCCCAAGGCGATTCGAGGACCTGATGACCGCTGCTGGAAAACGCTG	265
QY	586	CCCTCCCAAGCCCTTCATGTGAGGAAATTTGAAAATAATGATCACTTGAATGCGGTAC	645
Db	264	CCGAGAGATCGCCCTCGTCGATGCAATGATGATGAGGCGCTTATATGCACGAAATGTCMAAGAC	205
QY	646	TTTCCAGGACGATGATGACCATTTACAGTATCTCTGT	681
Db	204	TATACGGGGGCGAACAAAGGCCCTCGAATAATACATTT	169

## RESULT 10

US-03-270-76/16/15388/C  
; Sequence 15388, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
; FILE REFERENCE: File Reference: 7326-094

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? CURRENT APPLICATION NUMBER: US/09/270,767
? CURRENT FILING DATE: 1999-03-17
? NUMBER OF SEQ ID NOS: 62517
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO: 15388
? LENGTH: 507
? TYPE: DNA
? ORGANISM: Drosophila melanogaster
US-09-270-767-15388

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Query Match	15.2%	Score 104;	DB 4;	Length 507;
Best Local Similarity	58.9%;	Pred. No. 2.9e-24;		
Matches 198; Conservative	0;	Mismatches 135;	Indels 3;	Gaps 1

Qy	346	GGAGTGTGCTGGTGGAAAGGCACTTGAAGTTTGTGAAGTAGTAATTAACTGAGAAAATGT	405
Dd	501	GGATATGCCCTTGGATGGAGCGCCCGAGGCTCTTGGAAAGCTCCAAATAAACGAAAAAGGT	442
Qy	406	GACGCTTTCAGCTGGGGTATTATTCTTTGGGAAAGTAATAACGCTCGGAAACCCCTTGAT	465
Dd	441	GACATTTTTCAGCTGGGCAATTGTTCTATGGGAGGTTCTGTCCAGGAACCAACCCCTTTAA	382
Qy	466	GAGATGTGTGGCCAGCTTTCGGAATCAATGTGGGCTGTTCAATAGTAATCTGCACCA	525
Dd	381	GGCAT----CACAATGCTTACACCAATCACTGATGAAAATCTCAAGAGGTGAACGGCCGCG	325
Qy	526	CTGATTAATAAAATTTTACCTTAAGCCCATTTGAGACCTGATAGACTCGTGTGTGCTTAAGAT	585
Dd	324	CTGTGACCACTTGGCCCAAGCGCAATCGAGCACTGATGACCGACTGTGCTGGAAGAACGGTG	285
Qy	586	CCTTCCCAAGAGCCCTTCATATGAGGAAATGTGAAAATAATAGACTCACTTGAGCGGTAC	645
Dd	264	CCGAGAGATGGCCCGTCTGATGCAATGACATATGATGGCCGCTTAATGCAAGATGTTCAMAGAC	205
Qy	646	TTTTCAGAGACAGATAGGCACTTAACAGTATCTCTGT	681
Dd	204	TATACGGGGCGGACCAAGGCCCTGTGAATAATCAATTT	169

## RESULT 11

```

US-09-949-016-142616/c
/ Sequence 142616, Application US/09949016
/ Patent No. 681239
/ GENERAL INFORMATION:
/ APPLICANT: VENTNER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 142616
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
/ US-09-949-016-142616

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Query Match	10.5%;	Score 72;	DB 4;	Length 601;
Best Local Similarity	84.4%;	Pred. No. 1.5e-13;		
Matches 81; Conservative	0;	Mismatches 15;	Indels 0;	Gaps 0;

Qy	3	AGAGCTTCGACAGTATTCGCGTGAACATCTTAATTGTAAGCTTTATGAGACTCG	62
Db	96	ACAGCTTCGCACTTATCCGCGTGAACCATCTTAATTGTGAAGCTTTATGAGACCTCG	377
Qy	63	CTTGAATCCAGTGTCTTGTGATGGAATATGCTGA	98

Db 36 CTTGATCCAGTAGTTGTTACTTTTCATGTCGA 1

## RESULT 12

US-09-513-999C-3587  
; Sequence 3587, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59, US2, REG  
; CURRENT APPLICATION NUMBER: US/09/513, 999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 3587  
; LENGTH: 426  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 3..425  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 358  
; OTHER INFORMATION: m=a or c  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 392  
; OTHER INFORMATION: y=c or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 393  
; OTHER INFORMATION: b=c or g or t  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 119  
; OTHER INFORMATION: xaa=ala or glu  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 131  
; OTHER INFORMATION: xaa=ala or pro or ser  
US-09-513-999C-3587

Query Match 8.0%; Score 54.6; DB 4; Length 426;  
Best Local Similarity 48.3%; Pred. No. 8.2e-08;  
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 160 CACGCAATGAGTGGTGTGTTTACAGTGTCCCAAGAGAGGCTTATCTTACAGCATGCA 219  
DB 15 CACATTATGACCTGGGCCACTGATGTAGCAAGAAAGATGATTTTACATATGAGAGCT 74  
QY 220 CCCAAGGCGTAATTCACAGGAGCCTGAACACCAACCACTTCTGCTGTTGACAGGGGG 279  
DB 75 CTTGTCAGAGTATTCACAGAGACCTCAAGTCAAGAAAGCTTGTATAGCTCTGATGGA 134  
QY 280 ACAGTTCTAAAAATTTGTGATTTTGTACAGCCTGTGACATTCAGACACACATGACCAAT 339  
DB 135 GTAAGTGAAGATCTGAGACTTGTGCTGCTCGGTTCCATTAACATACACACATGATGCC 194  
QY 340 AACAGGGAGTGTCTGTGATGACACCTGAAGTTTGAAGTAGTAAATTAACAGTGA 399  
DB 195 TTGGTTGAACCTTCCCATGAGATGGCTCCAGAAAGTATCCAGAGTCTCCCTGTGCAGA 254  
QY 400 AAATGTACGCTTCAGCTGGGGTATTTATCTTTGGGAGATGATAACGGCTCGAAACCC 459  
DB 255 ACTGTGACACATATTCCTATGATGTGTCTCTGTGGGAGATGCTAAAGGAGGATCCCC 314

QY 460 TTGATGAGATTTGGTGG 476  
DB 315 TTAAAGTTTGAAGG 331

## RESULT 13

US-09-221-235-6  
; Sequence 6, Application US/09221235  
; Patent No. 6043040  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan  
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-050  
; CURRENT APPLICATION NUMBER: US/09/221,235  
; CURRENT FILING DATE: 1998-12-28  
; EARLIER APPLICATION NUMBER: 09/163,115  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1365  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1365)  
US-09-221-235-6

Query Match 8.0%; Score 54.6; DB 3; Length 1365;  
Best Local Similarity 48.3%; Pred. No. 1.6e-07;  
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 160 CACGCAATGAGTGGTGTGTTTACAGTGTCCCAAGAGAGGCTTATCTTACAGCATGCA 219  
DB 316 CACATTATGACCTGGGCCACTGATGTAGCAAGAAAGATGATTTTACATATGAGAGCT 375  
QY 220 CCCAAGGCGTAATTCACAGGAGCCTGAACACCAACCACTTCTGCTGTTGACAGGGGG 279  
DB 376 CTTGTCAGAGTATTCACAGAGACCTCAAGTCAAGAAAGCTTGTATAGCTCTGATGGA 435  
QY 280 ACAGTTCTAAAAATTTGTGATTTTGTACAGCCTGTGACATTCAGACACACATGACCAAT 339  
DB 436 GTAAGTGAAGATCTGAGACTTGTGCTGCTCGGTTCCATTAACATACACACATGATGCC 495  
QY 340 AACAGGGAGTGTCTGTGATGACACCTGAAGTTTGAAGTAGTAAATTAACAGTGA 399  
DB 496 TTGGTTGAACCTTCCCATGAGATGGCTCCAGAAAGTATCCAGAGTCTCCCTGTGCAGA 555  
QY 400 AAATGTACGCTTCAGCTGGGGTATTTATCTTTGGGAGATGATAACGGCTCGAAACCC 459  
DB 556 ACTGTGACACATATTCCTATGATGTGTCTCTGTGGGAGATGCTAAAGGAGGATCCCC 615  
QY 460 TTGATGAGATTTGGTGG 476  
DB 616 TTAAAGTTTGAAGG 632

## RESULT 14

US-09-221-928-6  
; Sequence 6, Application US/09221928  
; Patent No. 6121030  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan  
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-050  
; CURRENT APPLICATION NUMBER: US/09/221,928  
; CURRENT FILING DATE: 1998-12-28  
; EARLIER APPLICATION NUMBER: 09/163,115  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6

LENGTH: 1365  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1365)  
US-09-221-527-6

Query Match 8.0%; Score 54.6; DB 3; Length 1365;  
Best Local Similarity 48.3%; Pred. No. 1.6e-07;  
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

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QY 160 CACGCAATGATGGTGTGTTACAGTGTCCCAAGAGTGGCTTATCTTCACAGCATGCA 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 316 CACATTATGACCTGGGCCACTGATGTAGCCAAAGAAATGCAATTAATTAATGAGGCT 375
QY 220 CCCAAGGCGTAATTTACAGAGGACCTGAAACCACTTAACGCTGCTGGAGGGGG 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 376 CCTGTCAAGTGATTTCAAGAGACTCTCAAGTCAAGAAACGTTTATAGCTGCTGATGGA 435
QY 280 ACAGTTCTAAAAATTTGTGATTTGTGACAGCTGTGACATTCAGACACATGACCAAT 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 436 GTACTGAGATCTGTGACTTTGTGCTCTGCTTCATTAACATACACACATGTC 495
QY 340 AACAAAGGAGTGTGCTGTTGGATGGAACCTGAAGTTTGAAGTAGTAATTAACATGGA 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 496 TTGGTTGGAATTTCCCATGATGAGTGTCCAGAGATTAACAGATCTCCCTGTGTGAA 555
QY 400 AAATGTACGCTTTCAGCTGGGATTAATCTTTGGAGATGATTAACGCTCGAAACCC 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 556 ACTGTGACACATATCTCTATGTTGTGTCTCTGGAAGATGCTAACAGAGAGTCCCC 615
QY 460 TTTGATGAGATTTGTGG 476
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 616 TTAAAGTTTGAAG 632
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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## RESULT 15

US-09-221-527-6  
Sequence 6, Application US/09221527  
Patent No. 6146832  
GENERAL INFORMATION:  
APPLICANT: Acton, Susan  
TITLE OF INVENTION: NOVEL GSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
FILE REFERENCE: NMI-050  
CURRENT APPLICATION NUMBER: US/09/221,527  
CURRENT FILING DATE: 1998-12-28  
EARLIER APPLICATION NUMBER: 09/163,115  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 6  
LENGTH: 1365  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1365)  
US-09-221-527-6

Query Match 8.0%; Score 54.6; DB 3; Length 1365;  
Best Local Similarity 48.3%; Pred. No. 1.6e-07;  
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

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QY 160 CACGCAATGATGGTGTGTTACAGTGTCCCAAGAGTGGCTTATCTTCACAGCATGCA 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 316 CACATTATGACCTGGGCCACTGATGTAGCCAAAGAAATGCAATTAATTAATGAGGCT 375
QY 220 CCCAAGGCGTAATTTACAGAGGACCTGAAACCACTTAACGCTGCTGGAGGGGG 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 376 CCTGTCAAGTGATTTCAAGAGACTCTCAAGTCAAGAAACGTTTATAGCTGCTGATGGA 435
QY 280 ACAGTTCTAAAAATTTGTGATTTGTGACAGCTGTGACATTCAGACACATGACCAAT 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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```
Db 436 GTACTGAAGATCTGTACTTTGGTGTCTCGGTTCATTAACATACACACATGTCC 495
QY 340 AACAAAGGAGTGTGCTGCTGATGGAACCTGAAGTTTGAAGTAGTAATTAACATGGA 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 496 TTGGTTGGAATTTCCCATGATGAGTGTCCAGAGATTAACAGATCTCCCTGTGTGAA 555
QY 400 AAATGTACGCTTTCAGCTGGGATTAATCTTTGGAGATGATTAACGCTCGAAACCC 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 556 ACTGTGACACATATCTCTATGTTGTGTCTCTGGAAGATGCTAACAGAGAGTCCCC 615
QY 460 TTTGATGAGATTTGTGG 476
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 616 TTAAAGTTTGAAG 632
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Job time : 189.176 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2005, 17:26:02 ; Search time 732.527 Seconds  
(Without alignments)  
6043.588 Million cell updates/sec

Title: US-09-830-144-1\_COPY\_408\_1091

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Sequence: 1 gtgagagcttcgcagctatc.....cattacagctatcctgtcag 684

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IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

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3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
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18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*  
20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*  
21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*  
22: /cgn2\_6/ptodata/1/pubpna/US10J\_NEW\_PUB.seq.\*  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	684	100.0	1705	US-10-283-023-1	Sequence 1, Appli
2	684	100.0	1705	US-10-283-023-3	Sequence 3, Appli
3	684	100.0	1705	US-10-386-414-12	Sequence 12, Appli
4	684	100.0	1788	US-10-158-895-14	Sequence 14, Appli
5	684	100.0	1788	US-10-384-743-14	Sequence 14, Appli
6	684	100.0	2656	US-10-158-895-3	Sequence 3, Appli
7	684	100.0	2656	US-10-384-743-3	Sequence 3, Appli

8	684	100.0	2769	US-10-343-710-107	Sequence 107, App
9	65.4	9.6	1428	US-09-938-842A-882	Sequence 882, App
10	65.4	9.6	1428	US-09-938-842A-882	Sequence 882, App
11	64.4	9.4	2022	US-10-425-115-92866	Sequence 92866, A
12	61	8.9	1733	US-10-437-963-93253	Sequence 93253, A
13	56.8	8.3	476	US-09-732-627A-4894	Sequence 4894, Ap
14	56.6	8.3	1398	US-09-938-842A-633	Sequence 633, App
15	56.6	8.3	1398	US-09-938-842A-633	Sequence 633, App
16	56.2	8.2	732	US-10-767-701-10245	Sequence 10245, A
17	55.8	8.2	1953	US-10-424-599-53404	Sequence 53404, A
18	54.8	8.0	658	US-10-767-701-7653	Sequence 7653, Ap
19	54.6	8.0	863	US-10-425-114-6087	Sequence 6087, Ap
20	54.6	8.0	1063	US-10-106-698-2068	Sequence 2068, Ap
21	54.6	8.0	1365	US-09-757-982-6	Sequence 6, Appli
22	54.6	8.0	1365	US-10-786-501-6	Sequence 6, Appli
23	54.6	8.0	1456	US-10-425-114-36409	Sequence 36409, A
24	54.6	8.0	2120	US-10-352-674A-1	Sequence 1, Appli
25	54.6	8.0	2120	US-09-757-982-4	Sequence 4, Appli
26	54.6	8.0	2120	US-10-786-501-4	Sequence 4, Appli
27	54.6	8.0	2181	US-10-425-115-94149	Sequence 94149, A
28	54.6	8.0	2191	US-10-296-115-98	Sequence 98, Appli
29	54.6	8.0	2251	US-10-094-749-838	Sequence 838, Appli
30	54.6	8.0	2455	US-10-737-450-65	Sequence 65, Appli
31	54.6	8.0	3767	US-10-751-736-1	Sequence 1, Appli
32	54	7.9	782	US-10-425-114-18352	Sequence 18352, A
33	54	7.9	1926	US-10-425-114-32688	Sequence 22688, A
34	54	7.9	2029	US-10-425-114-34394	Sequence 34394, A
35	54	7.9	2050	US-10-425-115-84871	Sequence 84871, A
36	54	7.9	2793	US-10-425-115-16689	Sequence 16689, A
37	53.8	7.9	978	US-10-767-701-9215	Sequence 9215, Ap
38	53	7.7	1694	US-10-021-323-3324	Sequence 3324, Ap
39	53	7.7	1694	US-10-425-114-12718	Sequence 12718, A
40	53	7.7	2705	US-10-424-599-48931	Sequence 48931, A
41	52.6	7.7	715	US-10-424-599-43172	Sequence 43172, A
42	52.6	7.7	1219	US-10-424-599-130828	Sequence 130828, A
43	52	7.6	1051	US-10-424-599-130828	Sequence 9350, Ap
44	52	7.6	1737	US-10-767-701-9350	Sequence 13, Appli
45	52	7.6	1737	US-09-862-027-513	Sequence 13, Appli

#### ALIGNMENTS

RESULT 1  
US-10-283-023-1  
; Sequence 1, Application US/10283023  
; Publication No. US20030091573A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph M.  
; TITLE OF INVENTION: Methods and compositions for the  
; TITLE OF INVENTION: diagnosis and treatment of hematological disorders using  
; FILE REFERENCE: MP01-239P1RM  
; CURRENT APPLICATION NUMBER: US/10/283,023  
; PRIOR FILING DATE: 2002-10-29  
; PRIOR APPLICATION NUMBER: 60/335,044  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1705  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-283-023-1

Query Match 100.0%; Score 684; DB 14; Length 1705;  
Best Local Similarity 100.0%; Pred. No. 1.4e-207;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGAGCTTCGCGCACTTATCCGCTGTGAACCACTTAATTGTAAAGCTTTATGAGCC 60  
DB 226 GTAGAGCTTCGCGCACTTATCCGCTGTGAACCACTTAATTGTAAAGCTTTATGAGCC 285

QY 61 TCGTGAATCAGGTGTCTTGATGATAATGCTGAAGGGGCTCTTATATATATG 120  
DB 286 TCGTGAATCAGGTGTCTTGATGATAATGCTGAAGGGGCTCTTATATATATG 345  
QY 121 CTGCAATGAGTGAACCATTCGATATATATGCTGCGCCAGCAATGAGTGTGTTA 180  
DB 346 CTGCAATGAGTGAACCATTCGATATATATGCTGCGCCAGCAATGAGTGTGTTA 405  
QY 181 CAGTGTCCCAAGAGAGTGTATCTTCAAGCATGCAACCAAGCGCTAATTCACAG 240  
DB 406 CAGTGTCCCAAGAGAGTGTATCTTCAAGCATGCAACCAAGCGCTAATTCACAG 465  
QY 241 GACCTGAACCAACCAACTTACTGTGTGTGAGGGGGAGAGTCTTAAAAATTTGTAT 300  
DB 466 GACCTGAACCAACCAACTTACTGTGTGTGAGGGGGAGAGTCTTAAAAATTTGTAT 525  
QY 301 TTTGTGACAGCTGTGATTCAGACACACATGACCAATTAACAAGGGGAGTGTGTTG 360  
DB 526 TTTGTGACAGCTGTGATTCAGACACACATGACCAATTAACAAGGGGAGTGTGTTG 585  
QY 361 ATGCACTGAAGTCTTGAAGATGATTAATTAAGTGAAGTGAAGTGTGAGCTG 420  
DB 586 ATGCACTGAAGTCTTGAAGATGATTAATTAAGTGAAGTGAAGTGTGAGCTG 645  
QY 421 GGTATTTCTTTGGGAAGATGATTAAGTGAAGTGAAGTGAAGTGTGAGCTG 480  
DB 646 GGTATTTCTTTGGGAAGATGATTAAGTGAAGTGAAGTGAAGTGTGAGCTG 705  
QY 481 GCTTTCGAATCATGTGGGCTGTCATTAATGTACTGACACACATGATTAATAATTA 540  
DB 706 GCTTTCGAATCATGTGGGCTGTCATTAATGTACTGACACACATGATTAATAATTA 765  
QY 541 CCTAAGCCATTTGAGAGCTGATGATGCTGTGTGTGTTAAAGTCTTCCAGCGCCT 600  
DB 766 CCTAAGCCATTTGAGAGCTGATGATGCTGTGTGTGTTAAAGTCTTCCAGCGCCT 825  
QY 601 TCAATGAGGAATTTGTAATAATATGACTGATTAAGGAGTCTTCCAGAGAGAT 660  
DB 826 TCAATGAGGAATTTGTAATAATATGACTGATTAAGGAGTCTTCCAGAGAGAT 885  
QY 661 GAGCATTAACGATTCCTGTGAG 684  
DB 886 GAGCATTAACGATTCCTGTGAG 909

## RESULT 2

US-10-283-023-3  
; Sequence 3, Application US/10283023  
; Publication No. US20030091573A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph M.  
; TITLE OF INVENTION: Methods and compositions for the  
; TITLE OF INVENTION: diagnosis and treatment of hematological disorders using  
; FILE REFERENCE: MP101-239P1RM  
; CURRENT APPLICATION NUMBER: US/10/283,023  
; PRIOR FILING DATE: 2002-10-29  
; PRIOR APPLICATION NUMBER: 60/335,044  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1705  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1557)  
US-10-283-023-3

Query Match 100.0%; Score 684; DB 14; Length 1705;  
Best Local Similarity 100.0%; Pred. No. 1,4e-207;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGAGCTTGGGAGATTATCCGTGTGAACCATCTAATATGTAAAGCTTATGAGCC 60  
DB 226 GTAGAGCTTGGGAGATTATCCGTGTGAACCATCTAATATGTAAAGCTTATGAGCC 285  
QY 61 TCGTGAATCAGGTGTCTTGATGATAATGCTGAAGGGGCTCTTATATATATG 120  
DB 286 TCGTGAATCAGGTGTCTTGATGATAATGCTGAAGGGGCTCTTATATATATG 345  
QY 121 CTGCAATGAGTGAACCATTCGATATATATGCTGCGCCAGCAATGAGTGTGTTA 180  
DB 346 CTGCAATGAGTGAACCATTCGATATATATGCTGCGCCAGCAATGAGTGTGTTA 405  
QY 181 CAGTGTCCCAAGAGAGTGTATCTTCAAGCATGCAACCAAGCGCTAATTCACAG 240  
DB 406 CAGTGTCCCAAGAGAGTGTATCTTCAAGCATGCAACCAAGCGCTAATTCACAG 465  
QY 241 GACCTGAACCAACCAACTTACTGTGTGTGAGGGGGAGAGTCTTAAAAATTTGTAT 300  
DB 466 GACCTGAACCAACCAACTTACTGTGTGTGAGGGGGAGAGTCTTAAAAATTTGTAT 525  
QY 301 TTTGTGACAGCTGTGATTCAGACACACATGACCAATTAACAAGGGGAGTGTGTTG 360  
DB 526 TTTGTGACAGCTGTGATTCAGACACACATGACCAATTAACAAGGGGAGTGTGTTG 585  
QY 361 ATGCACTGAAGTCTTGAAGATGATTAATTAAGTGAAGTGAAGTGTGAGCTG 420  
DB 586 ATGCACTGAAGTCTTGAAGATGATTAATTAAGTGAAGTGAAGTGTGAGCTG 645  
QY 421 GGTATTTCTTTGGGAAGATGATTAAGTGAAGTGAAGTGAAGTGTGAGCTG 480  
DB 646 GGTATTTCTTTGGGAAGATGATTAAGTGAAGTGAAGTGAAGTGTGAGCTG 705  
QY 481 GCTTTCGAATCATGTGGGCTGTCATTAATGTACTGACACACATGATTAATAATTA 540  
DB 706 GCTTTCGAATCATGTGGGCTGTCATTAATGTACTGACACACATGATTAATAATTA 765  
QY 541 CCTAAGCCATTTGAGAGCTGATGATGCTGTGTGTGTTAAAGTCTTCCAGCGCCT 600  
DB 766 CCTAAGCCATTTGAGAGCTGATGATGCTGTGTGTGTTAAAGTCTTCCAGCGCCT 825  
QY 601 TCAATGAGGAATTTGTAATAATATGACTGATTAAGGAGTCTTCCAGAGAGAT 660  
DB 826 TCAATGAGGAATTTGTAATAATATGACTGATTAAGGAGTCTTCCAGAGAGAT 885  
QY 661 GAGCATTAACGATTCCTGTGAG 684  
DB 886 GAGCATTAACGATTCCTGTGAG 909

## RESULT 3

US-10-386-414-12  
; Sequence 12, Application US/10386414  
; Publication No. US20040006016A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapeller-Liberman, Rosana  
; APPLICANT: Rodison, Keith E.  
; APPLICANT: White, David  
; APPLICANT: Williamson, Mark W.  
; APPLICANT: Cook, William James  
; APPLICANT: Meyers, Rachel E.  
; APPLICANT: Macbeth, Kyle J.  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Chun, Miyoung  
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,  
; FILE REFERENCE: MP103-0210NMIM  
; CURRENT APPLICATION NUMBER: US/10/386,414  
; PRIOR FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: 09/426,282  
; PRIOR FILING DATE: 1999-10-25  
; PRIOR APPLICATION NUMBER: 09/668,266  
; PRIOR FILING DATE: 2000-09-22

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; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/254,037
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/833,082
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1705
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-386-414-12

Query Match      100.0%; Score 684; DB 17; Length 1705;
Best Local Similarity 100.0%; Pred. No. 1.4e-207;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGAGCTTGGGAGGATATCCCGTGTGAACATCCTAATATTTGTAACCTTTATGAGACC 60
DB 226 GTAGAGCTTGGGAGGATATCCCGTGTGAACATCCTAATATTTGTAACCTTTATGAGACC 285
QY 61 TGTGTAATCCAGTGTGCTTGTGTGATGTAATATGCTGAAGGGGCTCTTTATATATGTG 120
DB 286 TGTGTAATCCAGTGTGCTTGTGTGATGTAATATGCTGAAGGGGCTCTTTATATATGTG 345
QY 121 CTGATGATGCTGAACCATTCGCAATATATCTGTCGCCACCGCAATGATGTGGTTTA 180
DB 346 CTGATGATGCTGAACCATTCGCAATATATCTGTCGCCACCGCAATGATGTGGTTTA 405
QY 181 CAGTGTTCCTCAAGAGTGGCTTATCTTCAACAGCATGCAACCAAGCCCTAATTCACAGG 240
DB 406 CAGTGTTCCTCAAGAGTGGCTTATCTTCAACAGCATGCAACCAAGCCCTAATTCACAGG 465
QY 241 GACCTGAACAACCAACTTACTGCTGTGTGCAAGGGGGAACGTTCTAAAAATTTGTAT 300
DB 466 GACCTGAACAACCAACTTACTGCTGTGTGCAAGGGGGAACGTTCTAAAAATTTGTAT 525
QY 301 TTTGGTACAGCTGTGACATTCAGACACATGACCATTAACAAGGGAGTGTCTGG 360
DB 526 TTTGGTACAGCTGTGACATTCAGACACATGACCATTAACAAGGGAGTGTCTGG 585
QY 361 ATGGACCTGAAGTTTGAAGGTAGTAATTAACAGTGAATAATGAGTCTTCAAGCTGG 420
DB 586 ATGGACCTGAAGTTTGAAGGTAGTAATTAACAGTGAATAATGAGTCTTCAAGCTGG 645
QY 421 GGTATTAATCTTTGGGAAGTATAACGGCTCGAACCCTTTGATGAGATTGTGGCCCA 480
DB 646 GGTATTAATCTTTGGGAAGTATAACGGCTCGAACCCTTTGATGAGATTGTGGCCCA 705
QY 481 GCTTTCGAAATCATGTGGGCTGTTCATATATGTACTCCACCACTGATAAAAAATTTA 540
DB 706 GCTTTCGAAATCATGTGGGCTGTTCATATATGTACTCCACCACTGATAAAAAATTTA 765
QY 541 CCTAGGCCATTTAGAGGCTGATGACTGGTTGGTCTAAAGATCTTCCAGGAGCCCT 600
DB 766 CCTAGGCCATTTAGAGGCTGATGACTGGTTGGTCTAAAGATCTTCCAGGAGCCCT 825
QY 601 TCAATGAGGAATTTGTAAAAATTAATGACTCACTTGAATGCGGTACTTTTCAGAGCAAT 660
DB 826 TCAATGAGGAATTTGTAAAAATTAATGACTCACTTGAATGCGGTACTTTTCAGAGCAAT 885
QY 661 GAGCCATTACAGTATCTTGTGAG 684
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DB 886 GAGCCATTACAGTATCTTGTGAG 909

RESULT 4
US-10-158-895-14
; Sequence 14, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHITOMO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(1776)
US-10-158-895-14

Query Match      100.0%; Score 684; DB 13; Length 1788;
Best Local Similarity 100.0%; Pred. No. 1.4e-207;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGAGCTTGGGAGGATATCCCGTGTGAACATCCTAATATTTGTAACCTTTATGAGACC 60
DB 232 GTAGAGCTTGGGAGGATATCCCGTGTGAACATCCTAATATTTGTAACCTTTATGAGACC 291
QY 61 TGTGTAATCCAGTGTGCTTGTGTGATGTAATATGCTGAAGGGGCTCTTTATATATGTG 120
DB 292 TGTGTAATCCAGTGTGCTTGTGTGATGTAATATGCTGAAGGGGCTCTTTATATATGTG 351
QY 121 CTGATGATGCTGAACCATTCGCAATATATCTGTCGCCACCGCAATGATGTGGTTTA 180
DB 352 CTGATGATGCTGAACCATTCGCAATATATCTGTCGCCACCGCAATGATGTGGTTTA 411
QY 181 CAGTGTTCCTCAAGAGTGGCTTATCTTCAACAGCATGCAACCAAGCCCTAATTCACAGG 240
DB 412 CAGTGTTCCTCAAGAGTGGCTTATCTTCAACAGCATGCAACCAAGCCCTAATTCACAGG 471
QY 241 GACCTGAACAACCAACTTACTGCTGTGTGCAAGGGGGAACGTTCTAAAAATTTGTAT 300
DB 472 GACCTGAACAACCAACTTACTGCTGTGTGCAAGGGGGAACGTTCTAAAAATTTGTAT 531
QY 301 TTTGGTACAGCTGTGACATTCAGACACATGACCATTAACAAGGGAGTGTCTGG 360
DB 532 TTTGGTACAGCTGTGACATTCAGACACATGACCATTAACAAGGGAGTGTCTGG 591
QY 361 ATGGACCTGAAGTTTGAAGGTAGTAATTAACAGTGAATAATGAGTCTTCAAGCTGG 420
DB 592 ATGGACCTGAAGTTTGAAGGTAGTAATTAACAGTGAATAATGAGTCTTCAAGCTGG 651
QY 421 GGTATTAATCTTTGGGAAGTATAACGGCTCGAACCCTTTGATGAGATTGTGGCCCA 480
DB 652 GGTATTAATCTTTGGGAAGTATAACGGCTCGAACCCTTTGATGAGATTGTGGCCCA 711
QY 481 GCTTTCGAAATCATGTGGGCTGTTCATATATGTACTCCACCACTGATAAAAAATTTA 540
DB 712 GCTTTCGAAATCATGTGGGCTGTTCATATATGTACTCCACCACTGATAAAAAATTTA 771
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QY 541 CCTAAGCCCATTTGAGAGCCCTGTAAGTCTGTTGCTTAAAGATCTTCCAGGCCCT 600  
DB 772 CCTAAGCCCATTTGAGAGCCCTGTAAGTCTGTTGCTTAAAGATCTTCCAGGCCCT 831  
QY 601 TCAATGAGAGAAATTTGTAATTAATGACTGACTGATGCGGTACTTCCAGGAGCAT 660  
DB 832 TCAATGAGAGAAATTTGTAATTAATGACTGACTGATGCGGTACTTCCAGGAGCAT 891  
QY 661 GAGCCATTACAGTATCTTGTGAG 684  
DB 892 GAGCCATTACAGTATCTTGTGAG 915

## RESULT 5

US-10-384-743-14  
; Sequence 14, Application US/10384743  
; Publication No. US20030162228A1  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHIHIKO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/10/384,743  
; CURRENT FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: US/09/529,279  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: JP 9/290188  
; PRIOR FILING DATE: 1997-10-22  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 1788  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (7)..(1776)  
US-10-384-743-14

Query Match 100.0%; Score 684; DB 16; Length 1788;  
Best Local Similarity 100.0%; Pred. No. 1.4e-207;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGAGCTTGGGAGGATATCCCGTGTGAACCATCTTAATTTGTAAGCTTTATGAGCC 60  
DB 232 GTAGAGCTTGGGAGGATATCCCGTGTGAACCATCTTAATTTGTAAGCTTTATGAGCC 291  
QY 61 TGCCTGATCCAGTGTCTTGTGATGATGAATATGCTGAAGGGGCTCTTATATATG 120  
DB 292 TGCCTGATCCAGTGTCTTGTGATGATGAATATGCTGAAGGGGCTCTTATATATG 351  
QY 121 CTGCATGTGTCTGAACCATTTGATATGCTGCTCCAGCAATGAGTGTGTTA 180  
DB 352 CTGCATGTGTCTGAACCATTTGATATGCTGCTCCAGCAATGAGTGTGTTA 411  
QY 181 CAGTGTCCCAAGAGGGCTTATCTTCACAGATGCAACCCAAAGCGCTTAATTCAGG 240  
DB 412 CAGTGTCCCAAGAGGGCTTATCTTCACAGATGCAACCCAAAGCGCTTAATTCAGG 471  
QY 241 GACCTGAACCAACCAACTTACTGCTGTGTCAGGGGGGAGTCTTAATAATTTGTAT 300  
DB 472 GACCTGAACCAACCAACTTACTGCTGTGTCAGGGGGGAGTCTTAATAATTTGTAT 531  
QY 301 TTTGTGACGCTGTGATCATTCAGACACATGACCAATTAACAGGGGAGTGTCTTGG 360  
DB 532 TTTGTGACGCTGTGATCATTCAGACACATGACCAATTAACAGGGGAGTGTCTTGG 591  
QY 361 ATGGCAGCTGAAGTTTGTGAAGTATGTAATTAAGGAGAAATGACCTTTCAGCTGG 420  
DB 592 ATGGCAGCTGAAGTTTGTGAAGTATGTAATTAAGGAGAAATGACCTTTCAGCTGG 651

QY 421 GGTATTATCTTTGGGAGGATGAAGCGGCGAAACCTTTGATGATGATGTTGGCCCA 480  
DB 652 GGTATTATCTTTGGGAGGATGAAGCGGCGAAACCTTTGATGATGATGTTGGCCCA 711  
QY 481 GCTTTCCGAATCATGTGGCTGTTCTTAATTAATGTAATGTAACCAACATGTAATAAATTTA 540  
DB 712 GCTTTCCGAATCATGTGGCTGTTCTTAATTAATGTAATGTAACCAACATGTAATAAATTTA 771  
QY 541 CCTAAGCCCATTTGAGAGCCCTGTAAGTCTGTTGCTTAAAGATCTTCCAGGCCCT 600  
DB 772 CCTAAGCCCATTTGAGAGCCCTGTAAGTCTGTTGCTTAAAGATCTTCCAGGCCCT 831  
QY 601 TCAATGAGAGAAATTTGTAATTAATGACTGACTGATGCGGTACTTCCAGGAGCAT 660  
DB 832 TCAATGAGAGAAATTTGTAATTAATGACTGACTGATGCGGTACTTCCAGGAGCAT 891  
QY 661 GAGCCATTACAGTATCTTGTGAG 684  
DB 892 GAGCCATTACAGTATCTTGTGAG 915

## RESULT 6

US-10-158-895-3  
; Sequence 3, Application US/10158895  
; Publication No. US20020155624A1  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHIHIKO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/10/158,895  
; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: US/09/529,279  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: JP 9/290188  
; PRIOR FILING DATE: 1997-10-22  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 2656  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (183)..(1919)  
US-10-158-895-3

Query Match 100.0%; Score 684; DB 13; Length 2656;  
Best Local Similarity 100.0%; Pred. No. 1.7e-207;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGAGCTTGGGAGGATATCCCGTGTGAACCATCTTAATTTGTAAGCTTTATGAGCC 60  
DB 408 GTAGAGCTTGGGAGGATATCCCGTGTGAACCATCTTAATTTGTAAGCTTTATGAGCC 467  
QY 61 TGCCTGATCCAGTGTCTTGTGATGATGAATATGCTGAAGGGGCTCTTATATATG 120  
DB 468 TGCCTGATCCAGTGTCTTGTGATGATGAATATGCTGAAGGGGCTCTTATATATG 527  
QY 121 CTGCATGTGTCTGAACCATTTGATATGCTGCTCCAGCAATGAGTGTGTTA 180  
DB 528 CTGCATGTGTCTGAACCATTTGATATGCTGCTCCAGCAATGAGTGTGTTA 587  
QY 181 CAGTGTCCCAAGAGGGCTTATCTTCACAGATGCAACCCAAAGCGCTTAATTCAGG 240  
DB 588 CAGTGTCCCAAGAGGGCTTATCTTCACAGATGCAACCCAAAGCGCTTAATTCAGG 647  
QY 241 GACCTGAACCAACCAACTTACTGCTGTGTCAGGGGGGAGTCTTAATAATTTGTAT 300

Db 648 GACCTGAACCAACCAATTACTGCTGGTTCAGGGGGGACAGTTCTAAAAATTGGAT 707  
QY 301 TTTGGTACAGCTGTGACATTCACACACATGACCAATAACAAGGGAGTGTCTGG 360  
Db 708 TTTGGTACAGCTGTGACATTCACACACATGACCAATAACAAGGGAGTGTCTGG 767  
QY 361 ATGGACCTGAAGTTTGGAGGTATGATATGATGATGATGATGATGATGATGATGAT 420  
Db 768 ATGGACCTGAAGTTTGGAGGTATGATGATGATGATGATGATGATGATGATGAT 827  
QY 421 GGTATTAATCTTTGGAGGTATGATGATGATGATGATGATGATGATGATGATGAT 480  
Db 828 GGTATTAATCTTTGGAGGTATGATGATGATGATGATGATGATGATGATGATGAT 887  
QY 481 GCTTCCGAATCATGTGGGCTGTTCAATATGATGATGATGATGATGATGATGAT 540  
Db 888 GCTTCCGAATCATGTGGGCTGTTCAATATGATGATGATGATGATGATGATGAT 947  
QY 541 CCTAAGCCATTTGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 600  
Db 948 CCTAAGCCATTTGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1007  
QY 601 TCAATGAGGAATTTGGAATAATGATGATGATGATGATGATGATGATGATGATGAT 660  
Db 1008 TCAATGAGGAATTTGGAATAATGATGATGATGATGATGATGATGATGATGATGAT 1067  
QY 661 GAGCCATTACAGTATCTTGTGAG 684  
Db 1068 GAGCCATTACAGTATCTTGTGAG 1091

RESULT 7  
US-10-384-743-3  
; Sequence 3, Application US/10384743  
; Publication No. US20030162228A1  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHIIKO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/10/384,743  
; CURRENT FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: US/09/529,279  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: JP 9/290188  
; PRIOR FILING DATE: 1997-10-22  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 2656  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (183)..(1919)  
; US-10-384-743-3

Query Match 100.0%; Score 684; DB 16; Length 2656;  
Best Local Similarity 100.0%; Pred. No. 1.7e-207;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGAGCTTGGCAGTATCCCGTGTGAACCATCTTAATTTGTAAGCTTTATGAGCC 60  
Db 408 GTAGAGCTTGGCAGTATCCCGTGTGAACCATCTTAATTTGTAAGCTTTATGAGCC 467  
QY 61 TGCTTGAATCCAGTGTGCTTGTGATGATGATGATGATGATGATGATGATGATGAT 120  
Db 468 TGCTTGAATCCAGTGTGCTTGTGATGATGATGATGATGATGATGATGATGATGAT 527  
QY 121 CTGCAATGCTGGAACCATTTGATCTGCTGCCACGCAATGATGATGATGATGAT 180

Db 528 CTGCAATGCTGGAACCATTTGATCTGCTGCCACGCAATGATGATGATGATGAT 587  
QY 181 CAGTGTCCCAAGAGGCTTATCTTCAAGCATGCAACCCAAAGGCTAATTCACAGG 240  
Db 588 CAGTGTCCCAAGAGGCTTATCTTCAAGCATGCAACCCAAAGGCTAATTCACAGG 647  
QY 241 GACCTGAACCAACCAATTACTGCTGTGTCAGGGGGGACAGTTCTAAAAATTGGAT 300  
Db 648 GACCTGAACCAACCAATTACTGCTGTGTCAGGGGGGACAGTTCTAAAAATTGGAT 707  
QY 301 TTTGGTACAGCTGTGACATTCACACACATGACCAATAACAAGGGAGTGTCTGG 360  
Db 708 TTTGGTACAGCTGTGACATTCACACACATGACCAATAACAAGGGAGTGTCTGG 767  
QY 361 ATGGACCTGAAGTTTGGAGGTATGATGATGATGATGATGATGATGATGATGATGAT 420  
Db 768 ATGGACCTGAAGTTTGGAGGTATGATGATGATGATGATGATGATGATGATGATGAT 827  
QY 421 GGTATTAATCTTTGGAGGTATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
Db 828 GGTATTAATCTTTGGAGGTATGATGATGATGATGATGATGATGATGATGATGATGAT 887  
QY 481 GCTTCCGAATCATGTGGGCTGTTCAATATGATGATGATGATGATGATGATGAT 540  
Db 888 GCTTCCGAATCATGTGGGCTGTTCAATATGATGATGATGATGATGATGATGAT 947  
QY 541 CCTAAGCCATTTGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 600  
Db 948 CCTAAGCCATTTGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1007  
QY 601 TCAATGAGGAATTTGGAATAATGATGATGATGATGATGATGATGATGATGATGAT 660  
Db 1008 TCAATGAGGAATTTGGAATAATGATGATGATGATGATGATGATGATGATGATGAT 1067  
QY 661 GAGCCATTACAGTATCTTGTGAG 684  
Db 1068 GAGCCATTACAGTATCTTGTGAG 1091

RESULT 8  
US-10-343-710-107  
; Sequence 107, Application US/10343710  
; Publication No. US20040087478A1  
; GENERAL INFORMATION:  
; APPLICANT: GILLEN, Clemens  
; APPLICANT: WETZELS, Ingrid  
; APPLICANT: WENDEL, Stephan  
; APPLICANT: WEIHE, E.  
; APPLICANT: SCHAEFER, M. K.-H.  
; TITLE OF INVENTION: SCREENING METHOD  
; FILE REFERENCE: 029310.520220S  
; CURRENT APPLICATION NUMBER: US/10/343,710  
; CURRENT FILING DATE: 2003-09-17  
; PRIOR APPLICATION NUMBER: PCT/EP01/09011  
; PRIOR FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 157  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 107  
; LENGTH: 2769  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-343-710-107

Query Match 100.0%; Score 684; DB 16; Length 2769;  
Best Local Similarity 100.0%; Pred. No. 1.8e-207;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGAGCTTGGCAGTATCCCGTGTGAACCATCTTAATTTGTAAGCTTTATGAGCC 60  
Db 388 GTAGAGCTTGGCAGTATCCCGTGTGAACCATCTTAATTTGTAAGCTTTATGAGCC 447  
QY 61 TGCTTGAATCCAGTGTGCTTGTGATGATGATGATGATGATGATGATGATGATGAT 120

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Db 448 TCCTGATTCAGTGTGCTTGTGATGGAATAGCTGAAGGGGCTCTTTATATATG 507
Qy 121 CTGACGTGTGTAACCAATTCGCAATATATACCTGTGCCACGCAATAGTGTGTTA 180
Db 508 CTGACGTGTGTAACCAATTCGCAATATATACCTGTGCCACGCAATAGTGTGTTA 567
Qy 181 CAGTGTGCCAAGGAGTGTGTTATCTTCAAGCATGCAACCCAAAGGCTTAATTCAGG 240
Db 568 CAGTGTGCCAAGGAGTGTGTTATCTTCAAGCATGCAACCCAAAGGCTTAATTCAGG 627
Qy 241 GACCTGAACCAACCAACTTACTGTGTGAGGGGGAGACAGTCTTAAATTTGAT 300
Db 628 GACCTGAACCAACCAACTTACTGTGTGAGGGGGAGACAGTCTTAAATTTGAT 687
Qy 301 TTTGTATACGCTGTGATTCACACACATGACCAATTAACAAGGAGTGTGCTTG 360
Db 688 TTTGTATACGCTGTGATTCACACACATGACCAATTAACAAGGAGTGTGCTTG 747
Qy 361 ATGGACCTGAAGTTTGAAGATTAAGTAACTGTAAGTAAATGTAAGTCTTCACTGG 420
Db 748 ATGGACCTGAAGTTTGAAGATTAAGTAACTGTAAGTAAATGTAAGTCTTCACTGG 807
Qy 421 GGTATATCTTTGGGAAAGTATACCGGTGGAACCCCTTGTGATGATGTGGCCCA 480
Db 808 GGTATATCTTTGGGAAAGTATACCGGTGGAACCCCTTGTGATGATGTGGCCCA 867
Qy 481 GCTTCCGAATCATGTGGGCTGTTCATATAGTACTGACACCACTGATTAATAATTA 540
Db 868 GCTTCCGAATCATGTGGGCTGTTCATATAGTACTGACACCACTGATTAATAATTA 927
Qy 541 CCTAAGCCCATTTGAGAGCTGTGATCTGTGTGTCTTAAAGTCCCTCCAGCGCCCT 600
Db 928 CCTAAGCCCATTTGAGAGCTGTGATCTGTGTGTCTTAAAGTCCCTCCAGCGCCCT 987
Qy 601 TCAATGAGGAATTTGAAATATATGACTTATGCGGTACTTTCCAGAGCAGAT 660
Db 988 TCAATGAGGAATTTGAAATATATGACTTATGCGGTACTTTCCAGAGCAGAT 1047
Qy 661 GAGCCATTACAGTATCCTGTCCAG 684
Db 1048 GAGCCATTACAGTATCCTGTCCAG 1071

```

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RESULT 9
US-09-938-842A-882
; Sequence 882, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 882
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-882

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Query Match 9.6%; Score 65.4; DB 9; Length 1428;  
Best Local Similarity 49.3%; Pred. No. 1.1e-09;

```

Matches 171; Conservative 0; Mismatches 176; Indels 0; Gaps 0;
Qy 338 ATAAAGAGGGAGTGTGCTGTGATGAGCACTGAAGTTTTTGAAGTACTAATTACAGTC 397
Db 956 ATAACTAGTGAACCTTTATAGTGTGATGCACTGAAGTTTTTAAACGATACACATGAC 1015
Qy 398 AAAATGTGACGTCTTCACTGCGGTATTAATCTTTGGAGAGTGAATTAACGCTCGGAAC 457
Db 1016 GGAAGTGCATGTTTATAGTTTGGACTTCTTTATGGAAGTAATGTAGTGAAGACTTC 1075
Qy 458 CTTTATGATGATGTGTGCCCCAGCTTCCGATCATGTGGCTGTTCATAATGTGACTC 517
Db 1076 CATATGAGAGTGAATTTGTCTGAACAAATGTGCTTACGCACTTATATCAAGAAATTA 1135
Qy 518 GACCACTCATGATTAATAATTTAACCCTTAAGCCATTTAGAGCCTGATGACTGTGTGCT 577
Db 1136 GGCACATTTATCCAGACGATTTCTCCAGCGCCATGAAGAGCTGATCCAGCGATGTGT 1195
Qy 578 CTAAAGATCTTCCAGCGCCCTTCAATGAGAGAAATGTGAAATTAATGACTCACTTGA 637
Db 1196 CATGCAACACAGACAAGAGACCGGAATCTGGCAGATTTGTCAAGTGTGGAACATTTCA 1255
Qy 638 TGGGTACTTTCAGAGAGCAGATGAGCCATTAAGTATCCTTGTAG 684
Db 1256 AAGATCTTAACAAGCAAGGAAATTAATCTTTTACTTACGACG 1302

```

```

RESULT 10
US-09-938-842A-882
; Sequence 882, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 882
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-882

```

Query Match 9.6%; Score 65.4; DB 11; Length 1428;  
Best Local Similarity 49.3%; Pred. No. 1.1e-09;  
Matches 171; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

```

Qy 338 ATAAAGAGGGAGTGTGCTGTGATGAGCACTGAAGTTTTTGAAGTACTAATTACAGTC 397
Db 956 ATAACTAGTGAACCTTTATAGTGTGATGCACTGAAGTTTTTAAACGATACACATGAC 1015
Qy 398 AAAATGTGACGTCTTCACTGCGGTATTAATCTTTGGAGAGTGAATTAACGCTCGGAAC 457
Db 1016 GGAAGTGCATGTTTATAGTTTGGACTTCTTTATGGAAGTAATGTAGTGAAGACTTC 1075
Qy 458 CTTTATGATGATGTGTGCCCCAGCTTCCGATCATGTGGCTGTTCATAATGTGACTC 517
Db 1076 CATATGAGAGTGAATTTGTCTGAACAAATGTGCTTACGCACTTATATCAAGAAATTA 1135
Qy 518 GACCACTCATGATTAATAATTTAACCCTTAAGCCATTTAGAGCCTGATGACTGTGTGCT 577
Db 1136 GGCACATTTATCCAGACGATTTCTCCAGCGCCATGAAGAGCTGATCCAGCGATGTGT 1195
Qy 578 CTAAAGATCTTCCAGCGCCCTTCAATGAGAGAAATGTGAAATTAATGACTCACTTGA 637
Db 1196 CATGCAACACAGACAAGAGACCGGAATCTGGCAGATTTGTCAAGTGTGGAACATTTCA 1255
Qy 638 TGGGTACTTTCAGAGAGCAGATGAGCCATTAAGTATCCTTGTAG 684
Db 1256 AAGATCTTAACAAGCAAGGAAATTAATCTTTTACTTACGACG 1302

```

QY 578 CTAAGATCTCTCCAGCGCCCTTCAATGAGGAATTTGAAATATGACTCACTGA 637  
 DB 1196 CATCGCAACAGCAACAAAGACCGGAATCTGGCGATTTGCAAGGTTGGAACTTTCA 1255  
 QY 638 TGGGTAATCTTCCAGAGCAGATGAGCCATTACAGTATCTTGTGAC 684  
 DB 1256 AGAAGTCTTAACAGGAGGAAAGAACTTATATCTTTACTAGCCAG 1302

## RESULT 11

US-10-425-115-92866  
 ; Sequence 92866, Application US/10425115  
 ; Publication No. US20040214272A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
 ; FILE REFERENCE: 38-21(53222)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,115  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 369326  
 ; SEQ ID NO 92866  
 ; LENGTH: 2022  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: MRT4577\_184684C.1  
 US-10-425-115-92866

Query Match 9.4%; Score 64.4; DB 20; Length 2022;  
 Best Local Similarity 50.5%; Pred. No. 2.6e-09;  
 Matches 211; Conservative 0; Mismatches 201; Indels 6; Gaps 2;

QY 209 ACAGCATGCAACCAAGCGCTAATTCAGAGGACCTGAAACCAACTTACTGCTGG 268  
 DB 1202 ACTACCTGCAACCAAGCAATTAATTCACCGCATCTCAAGACTGCAAACTCTTCATGG 1261  
 QY 269 TTGCA---GGGGGACAGTTCTTAATAATTTGGAATTTGGTACAGCGCTGATCAATTCGA 325  
 DB 1262 ATGAAAACAAAGTTGTAAGGTTGCAACTTTGGTGGTCAAGATGAAGACCAATTCG 1321  
 QY 326 CACACATGACCAATTAACAAAGGAGTGTGCTGCTGGATGCACTGAAATTTTGAAGGTA 385  
 DB 1322 GAGTGAATCTGCAAGAACTGAACTTACCGTTGATGCACTGAGGTCATAGAACTA 1381  
 QY 386 GTAATTACAGTGAATAATGTACGCTTCAAGCTGGGATTAATTTCTTTGGAAAGTATTA 445  
 DB 1382 AGCCCTAGCATCAAAAGCGATGTTTGTAGCTTGTGATTTCTTTGGGAACTGCTAA 1441  
 QY 446 CGCGTGGAAACCTTTGATGATGATTTGGGCGCCAGCTTCCGATCATGTGGGCTGTTTC 505  
 DB 1442 CCGGAGAGATCCC--TTACAGTACCTTACACCACTGCAAGCAAGCAATAGTGTGTTTC 1498  
 QY 506 ATAAATGACTGACCAACCACTGATTAATAAATTTTACCTAAGCCATTGAGAGCTGATGA 565  
 DB 1499 AGAAGGATTAAGGCAACAAATTCACAAAGACACACATCCCAAGTCTATCGAGCTTCTTC 1558  
 QY 566 CTCGTTGTTGTTAAGATCTTCCAGCGCCCTTCAATGAGGAAATTTGAAAT 623  
 DB 1559 AGAATGTTGGATGAGATCAGCTGAGAGGCGGAGCTTCTCGAGATATCGAGAT 1616

## RESULT 12

US-10-437-963-93253  
 ; Sequence 93253, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua  
 APPLICANT: Cao, Yongwei  
 APPLICANT: Wu, Wei  
 APPLICANT: Boukharov, Andrey A.  
 APPLICANT: Barabuk, Brad  
 APPLICANT: Li, Ping  
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
 FILE REFERENCE: 38-21(53221)B  
 CURRENT APPLICATION NUMBER: US/10/437,963  
 CURRENT FILING DATE: 2003-05-14  
 NUMBER OF SEQ ID NOS: 204966  
 SEQ ID NO 93253  
 LENGTH: 1733  
 TYPE: DNA  
 ORGANISM: Oryza sativa  
 FEATURE:  
 NAME/KEY: unsure  
 LOCATION: (1)..(1733)  
 OTHER INFORMATION: unsure at all n locations  
 FEATURE:  
 OTHER INFORMATION: Clone ID: PAT\_MRT4530\_91656C.1  
 US-10-437-963-93253

Query Match 8.9%; Score 61; DB 19; Length 1733;  
 Best Local Similarity 52.9%; Pred. No. 3e-08;  
 Matches 155; Conservative 0; Mismatches 135; Indels 3; Gaps 1;

QY 331 ATGACCAATTAACAAAGGAGTGTGCTGATGAGGACCTGAAAGTTTGAAGTATGAT 390  
 DB 1183 ATGCTGACAGAGATGGAACCTTATCGTTGATGAGGACCTGAGTCAATGAACAAAGCC 1242  
 QY 391 TACAGTAAATATGACGCTTTCAGCTGGGTTATTTCTTTGGGAAGTATACGGGT 450  
 DB 1243 TATATATATTAAGCAAGATGTTTGAAGCTTTGTAATTTCTATAGAGGCTCTAATCTGGC 1302  
 QY 451 CGGAACCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 510  
 DB 1303 AAGTATCCCT--ATGATTAATTAACCACTTACCAAGCAAGCAAGCAAGCAAGCAAGCA 1359  
 QY 511 GGTACTGACCAACCACTGATTAATAAATTTTAACTTAAGCCATTGAGAGCTGATGATGAT 570  
 DB 1360 GGCCTTGAACCAACCAATTCGAAAGATACGACCCCAAGCTGTGATGATGATGATGAT 1419  
 QY 571 TGTGTTGTTAAGATCTCTCCAGCGCCCTTCAATGAGGAAATTTGAAAT 623  
 DB 1420 TGCTGGATGAGATCTCTGTAAGAGGCTGATCTTCTCCAGATATCGAGAT 1472

## RESULT 13

US-09-732-627A-4894  
 ; Sequence 4894, Application US/09732627A  
 ; Publication No. US20040123338A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fincher, Karen L.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
 ; FILE REFERENCE: 38-21(51770)B  
 ; CURRENT APPLICATION NUMBER: US/09/732,627A  
 ; CURRENT FILING DATE: 2000-12-08  
 ; NUMBER OF SEQ ID NOS: 4930  
 ; SEQ ID NO 4894  
 ; LENGTH: 476  
 ; TYPE: DNA  
 ; ORGANISM: Gossypium hirsutum  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: LIB3493-039-P1-M1-E4  
 US-09-732-627A-4894

Query Match 8.3%; Score 56.8; DB 11; Length 476;  
 Best Local Similarity 53.4%; Pred. No. 3.4e-07;  
 Matches 143; Conservative 0; Mismatches 122; Indels 3; Gaps 1;

QY	206	TTCAAGCATGCAACCCNAAGCGCTAATTCACAGGACCTGAAACCAACCAACTACTGC	265
Db	206	TGCAGTACCTTCATTCACAGGAATACTTCAACAGGATCTCAAAATCAGAAATTTTACTCC	265
QY	266	TGCTTGACGGGGGACAGTCTTAAAAATTTTGATTTTGGTACAGCCCTGTGACATTCAGA	325
Db	266	TTGAGAAAGATATGTGTGTGAAGGTGGACAGATTTTGGTATTTTCAGCTTAAATCTCAGT	325
QY	326	CACACATGACCA--TAACAAGGGAGTGTGCTTGATGGCACTGAAGTTTYYGAG	382
Db	326	GTGTGATGTGCAAAAGGATTTACAGTACTTATCGGTGATGGCACTGAATGATTTAAAG	385
QY	383	GTAGTAAATTCAGTGAAGAAATATGACGCTTCAGCTGGGGTATATTTCTTTGGGAAGTGA	442
Db	386	AGAAACATCATCAAGAAAGTAAGTGTGTTACAGTTTTGGCATAGTCTCTTTGGAGCTTT	445
QY	443	TAACGCGTCGGAAACCTTTGATGAGAT	470
	446	TAACGGCTTTGACACCATTTGACAAAT	473

```

RESULT 14
US-09-938-842A-633
; Sequence 633, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 633
; LENGTH: 1398
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
;S-09-938-842A-633

```

Query Match	8.3%	Score 56.6	DB 9	Length 1398
Best Local Similarity	52.3%	Pred. No. 6.9e-07		
Matches 150	Conservative 0	Mismatches 134	Indels 3	Gaps 1
QY	186	TTCCCAAGAGATGGCTTATCTTCACAGATGAACCCAAAGCGCTAAATTCACAGGGACCT	245	
Db	714	TGCAGAAATGCTCTCTGCAGTTTCCCATCTCCATGAGAAAGCATATATGCACAGATCT	773	
QY	246	GAAACCAACAACTTACTCTGCTGTTCAGGGGGGACAG--TCTAAAAATTTGTGATTT	302	
Db	774	GAAACCCGAAACACTACTCATGATGATACAGATGGCCACCTGATGCTAACAGATTTTGGTTT	833	
QY	303	TGATACAGCCCTGTGACATTCAGACACATGATACCAATTAACAAGGGGAGTGCTGTGGAT	362	
Db	834	AGCAAAAGAAATTTGAAGAAACACAGATCAAACTCCATGTGCGGAATACAGAGTATAT	893	
QY	363	GGACCCGGAAGTTTGAAGGTAGTAAATACATGGAAGAAATGTGACGCTTTCAGCTGGGG	422	
Db	894	GGACCTGAATTTGTGAGGAAAAAGACATGATTAAGACACTCACTGGTGGAGCGTAGG	953	
QY	423	TATTAATCTTTGGAGTGATTAACGCGTCGAAACCTTTGATAGA	469	
Db	954	GATTCCTCTGATAGATGCTCAAGGAAAGCCACCGCTTTTCGGGA	1000	

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RESULT 15
US-09-938-842A-633
; Sequence 633, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227, 866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264, 647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300, 111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 633
; LENGTH: 1398
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-633

```

Query Match	8.3%;	Score 56.6;	DB 11;	Length 1398;
Best Local Similarity	52.3%;	Pred. No. 6.9e-07;		
Matches 150;	Conservative	0;	Mismatches 134;	Indels 3; Gaps 1
QY	186	TTCCAGAGAGGGCTTATCTTCAACAGATGCAACCCAAAGCCCTATTCAACGGGACCT	245	
Db	714	TGCAGAAATCGTCTGTGCAGTTTCCCATCTCATGAGAAAGCATATGTACACGAGATCT	773	
QY	246	GAACACCAAACTTACGTCTGTGTGACGGGGGACG---TCTTAAATTTTGTGATTT	302	
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Job time : 735.527 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 2, 2005, 17:28:02 ; Search time 22.3378 Seconds  
(without alignments)  
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Searched: 513545 seqs, 74649064 residues  
Total number of hits satisfying chosen parameters: 1027090

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1252	100.0	579	US-10-158-895-4	Sequence 4, Appli
3	1252	100.0	590	US-09-529-279-15	Sequence 15, Appli
4	1252	100.0	590	US-10-158-895-15	Sequence 15, Appli
5	1252	100.0	633	US-09-949-016-9902	Sequence 9902, Ap
6	392.5	31.3	663	US-09-949-016-7198	Sequence 7198, Ap
7	371	29.6	455	US-09-221-235-5	Sequence 5, Appli
8	371	29.6	455	US-09-221-928-5	Sequence 5, Appli
9	371	29.6	455	US-09-221-527-5	Sequence 5, Appli
10	371	29.6	455	US-09-221-236-5	Sequence 5, Appli
11	371	29.6	455	US-09-221-416-5	Sequence 5, Appli
12	371	29.6	455	US-09-221-245-5	Sequence 5, Appli

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14	371	29.6	455	3	US-09-221-528-5	Sequence 5, Appli
15	371	29.6	455	3	US-09-593-553-5	Sequence 5, Appli
16	371	29.6	455	3	US-09-221-237-5	Sequence 2, Appli
17	371	29.6	455	4	US-09-399-588-2	Sequence 2, Appli
18	371	29.6	455	4	US-09-757-982-5	Sequence 5, Appli
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## ALIGNMENTS

RESULT 1  
US-09-529-279-4  
Sequence 4, Application US/09529279  
Patent No. 6451617  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/09/529, 279  
CURRENT FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-529-279-4

Alignment Scores:  
Pred. No.: 2.36e-144  
Score: 1252.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 4  
Gaps: 0

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RESULT 2
US-10-158-895-4
; Sequence 4, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158, 895
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529, 279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-4

Alignment Scores:
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Score: 1252.00 Matches: 228
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

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Db      296 GluProLeuGlnTyrProCysGln 303

RESULT 3
US-09-529-279-15
; Sequence 15, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529, 279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
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NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 590  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-529-279-15

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## RESULT 4

US-10-158-895-15  
Sequence 15, Application US/10158895  
Patent No. 6551840  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIIHIKO

APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF- $\beta$ 2 INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 590  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-15

## Alignment Scores:

Pred. No.:	2,39e-144	Length:	590
Score:	1252.00	Matches:	228
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

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QY 61 TGCTTGAATCCAGTGTCTTGTGATGAAATATGCTGAAGGGGCTTTTATATATATG 120
   |||
Db 96 CysLeuAsnProValCysLeuValMetGluTyAlaGluGlySerLeuTyAsnVal 115
QY 121 CTGCATGCTGCTGAACCATTCGCAATATTATCTGCTGCCACGCAATGAGTTGTTTA 180
   |||
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RESULT 5
US-09-949-016-9902
/ Sequence 9902, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9902
/ LENGTH: 633
/ TYPE: PRN
/ ORGANISM: Human
US-09-949-016-9902

Alignment Scores:
Pred. No.: 2,47e-144 Length: 633
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

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QY 1 GTGAGCTTGGGAGGATATCCCGTGAACCACTTAAATTTGTAAGCTTTATGAGCC 60
Db 130 ValGlnLeuArgGlnLeuSerArgValAsnHisProAsnIleValIleuTyrgIylala 149
QY 61 TGCTTGAATCCAGTGTGTCTTGTGATGATATGCTGAAGGGGCTCTTTATATATG 120
Db 150 CysLeuAsnProValCysLeuValMetGluTyrlleGluIlyserIeuTyraVal 169
QY 121 CTGCAATGCTGCTGAACCATTTATTAATCTGCTGCCCAAGCAATGAGTGTGTTA 180
Db 170 LeuHisGlyAlaGlnProLeuProTyrlThrAlaAlaHisAlaMetSerTrpCysLeu 189
QY 181 CAGTGTTCACAGAGGCTTATCTTCAACAGATCAACCCAAACGCTTATTCACAG 240
Db 190 GlnCysSerGlnIylalaIatIyrlLeuHisSerMetGlnProValAlaLeuIleHisArg 209
QY 241 GACCTGAAAACCAAACTTACTGTGTGTTCAGGGGAGCAAGTCTTAAAAATTTGTAT 300
Db 210 AspIleuIleProProAsnLeuLeuValAlaGlyIylThrValLeuIleCysAsp 229
QY 301 TTGTGTACAGCCGTGACATTTGACACATGACATGACATTAACAGGGAGTGTCTGG 360
Db 230 PheGlyIylThrAlaCysAspIleGlnTrHisMetThrAsnAsnIleGlySerAlaIatPr 249
QY 361 ATGGACCTGAAGTTTGTGAAGTATTAATCAAGTGAATAATGACGCTTTCAGCTGG 420
Db 250 MetAlaProGlnValPheGlnIlySerAsnIylrSerGlnIylCysAspValPheSerTrp 269
QY 421 GGAATATCTTTGGGAAGTATTAACGCGTGGAAAACCTTTGATGAGATTGTGGCCA 480
Db 270 GlyIleIleLeuTrpGlnValIleThrArgArgIylsProPheAspGlnIleGlyIylPro 289
QY 481 GCTTCCGATCATGTGGGCTGTTCATATATGATACCGACCACTGATTAATAAATTTA 540
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Db 290 AlaPheArgIleMetTrpAlaValHisAsnGlyIylArgProProLeuIleIysAsnLeu 309
QY 541 CTTAAGCCCATTTAGAGCTGATGACTGTGTGTGTTAAAGATCTTCCAGGCGCT 600
Db 310 ProlsProIleGlnIleuSerMetThrArgCysTrpSerIylAspProSerGlnArgPro 329
QY 601 TCAATGAGAAATTTGAAATTAATGACTCACTGATGGGTACTTTCAGACACAT 660
Db 330 SerMetGlnIylleValIylsIleMetTrHisLeuMetArgIylrPheProGlyAlaAsp 349
QY 661 GAGCATTACAGTATCTTGACG 684
Db 350 GlnProLeuGlnTyProCysGln 357
RESULT 6
US-09-949-016-7198
/ Sequence 7198, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7198
/ LENGTH: 663
/ TYPE: PRN
/ ORGANISM: Human
US-09-949-016-7198

Alignment Scores:
Pred. No.: 6,38e-39 Length: 663
Score: 392.50 Matches: 88
Percent Similarity: 56.68% Conservative: 35
Best Local Similarity: 40.55% Mismatches: 77
Query Match: 31.35% Indels: 17
DB: 4 Gaps: 6

US-09-830-144-1_COPY_408_1091 (1-684) x US-09-949-016-7198 (1-663)
QY 4 GAGCTTGGGAGGATATCCCGTGAACCACTTAAATTTGTAAGCTTTATGAGCCTGC 63
Db 198 GlnIleAlaArgLeuPheGlyAlaLeuGlnHisProAsnIleIleAlaLeuArgIylalaCys 217
QY 64 TTGAATCA-----GTGTGCTTGTGATGATATGCTGAAGGGGCTCTTATATAT 117
Db 218 LeuAsnProProHisIleuCysLeuValMetGlnIylrAlaArgGlyIylAlaLeuSerArg 237
QY 118 GTGCTGATGGTGTGAACCATTTGATTAATTAATCTGCTGCCCAAGCAATGAGTGTGT 177
Db 238 ValLeuAlaGlyArgValrProHisIleVal-----LeuValAsnTrpAla 253
QY 178 TTACAGTGTTCACAGAGGCTTATCTTCAACAGATCAACCCAAACGCTTATTCAC 237
Db 254 ValGlnValAlaArgGlyMetAsnIylrLeuHisAsnAspAlaProIleIleHis 273
QY 238 AGGACCTGAACCAACCACTTACTGTCTGTT-----GCAGGG 276
Db 274 ArgAspIleuIylsSerIleAsnIleLeuIleLeuGlnAlaIleGlnAsnHisAsnLeuAla 293
QY 277 GCGACATTTTAAATTTGTGATTTTGTGACGCTGTGAC---ATTGACACACATG 333
Db 294 AspThrValLeuIylsIleThrAspPheGlyLeuAlaArgGlnTrpHisIylsThrThrIyls 313
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Db 149 IleCyAspPheGly---AlaSerArgPheHisAsnHisThrThiHisMetSerLeuVal 167  
QY 346 GGAAGTCTGCTTGGATGACCTGAAAGTTTGGAAAGTAGTAATTAACAGTAAATATG 405  
Db 168 GylThrPheProThrMetAlaProGluValIleGlnSerLeuProValSerGluThrCys 187  
QY 406 GAGCTCTCAGCTGGGGATATATCTTTGGGAAGTAAACCGCTCGAAACCTTTGAT 465  
Db 188 AspThrTySerTyrGlyValValLeuThrGluMetLeuThrArgGluValProPheLys 207  
QY 466 GAGATTGTGGCCCACTTTCGAAATCATGTG3---GCTGTTCAATATGTAAGTACGACCA 522  
Db 208 GlyLeuGluGly-----LeuGlnValAlaTrpLeuValValGlnLysAsnGluThrGlu 225  
QY 523 CCACGTGATAAAAATTTCCTTAAGCCCATTTGAAGCTGATGACTGCTGTTGGCTTAA 582  
Db 226 ThrIleProSerSerCysProArgSerPheAlaGluLeuHisGlnCysTrpGluVala 245  
QY 583 GATCCTTCCAGCGCCCTTCAATGGAGGAATTTGAAATTAATG 627  
Db 246 AspAlaLysLysArgProSerPheLysGlnIleIleSerIleLeu 260

## RESULT 9

US-09-221-527-5  
/ Sequence 5, Application US/09221527  
/ Patent No. 6146832  
/ GENERAL INFORMATION:  
/ APPLICANT: Acton, Susan  
/ TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
/ FILE REFERENCE: WMI-050  
/ CURRENT APPLICATION NUMBER: US/09/221,527  
/ EARLIER FILING DATE: 1998-12-28  
/ EARLIER APPLICATION NUMBER: 09/163,115  
/ NUMBER OF SEQ ID NOS: 15  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 5  
/ LENGTH: 455  
/ TYPE: PR  
/ ORGANISM: Homo sapiens  
US-09-221-527-5

Alignment Scores:  
Pred. No.: 2,3e-36 Length: 455  
Score: 371.00 Matches: 81  
Percent Similarity: 56.28% Conservative: 40  
Best Local Similarity: 37.67% Mismatches: 80  
Query Match: 29.63% Indels: 14  
Gaps: 8

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-09-221-527-5 (1-455)

QY 4 GAGCTTCGGCAGTTATCCCGTGGAAACCATCTTAATTTGTAAGCTTATGAGCCTGC 63  
Db 53 GluAlaGluIleLeuSerValIleuSerHisArgAsnIleIleGlnPheTyrGlyValIle 72  
QY 64 TTGAATCCA-----GTGTCTTGTGATGATATGCTGAAGGGGGCTTTATATAT 117  
Db 73 LeuGluProProAsnTyrGlyIleValThrGluTyrAlaSerLeuGlySerLeuTyrAsp 92  
QY 118 GTGCTGCATGCT-----GCTGAACCATTTGCCATATTAATCTGCTGCCACGAATGAGT 171  
Db 93 TyrIleAsnSerAsnArgSerGluGluMet-----AspMetAspHisIleMetThr 109  
QY 172 TGGTGTTCACAGTGTCCCAAGAGAGTGGCTTATCTTACAGCATGCAACCAAGCGCTA 231  
Db 110 TrpAlaThrAspValAlaLysGlyMetHisTyrLeuHisMetGluAlaProValLysVal 129  
QY 232 ATTTCACAGGAGCTGAAACCAACCACTTAAGCTGCTGGTTCAGGGGGGACAGTTCTAAA 291  
Db 130 IleHisArgAspLeuLysSerArgAsnValIleAlaLysArgLys-----ValLeuLys 148  
QY 292 ATTGTGATTTTGTGACAGCTGTGACATTCAGACACATGACCAATTAACAAG----- 345

Db 149 IleCyAspPheGly---AlaSerArgPheHisAsnHisThrThiHisMetSerLeuVal 167  
QY 346 GGAAGTCTGCTTGGATGACCTGAAAGTTTGGAAAGTAGTAATTAACAGTAAATATG 405  
Db 168 GylThrPheProThrMetAlaProGluValIleGlnSerLeuProValSerGluThrCys 187  
QY 406 GAGCTCTCAGCTGGGGATATATCTTTGGGAAGTAAACCGCTCGAAACCTTTGAT 465  
Db 188 AspThrTySerTyrGlyValValLeuThrGluMetLeuThrArgGluValProPheLys 207  
QY 466 GAGATTGTGGCCCACTTTCGAAATCATGTG3---GCTGTTCAATATGTAAGTACGACCA 522  
Db 208 GlyLeuGluGly-----LeuGlnValAlaTrpLeuValValGlnLysAsnGluThrGlu 225  
QY 523 CCACGTGATAAAAATTTCCTTAAGCCCATTTGAAGCTGATGACTGCTGTTGGCTTAA 582  
Db 226 ThrIleProSerSerCysProArgSerPheAlaGluLeuHisGlnCysTrpGluVala 245  
QY 583 GATCCTTCCAGCGCCCTTCAATGGAGGAATTTGAAATTAATG 627  
Db 246 AspAlaLysLysArgProSerPheLysGlnIleIleSerIleLeu 260

## RESULT 10

US-09-221-236-5  
/ Sequence 5, Application US/09221236  
/ Patent No. 6146841  
/ GENERAL INFORMATION:  
/ APPLICANT: Acton, Susan  
/ TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
/ FILE REFERENCE: WMI-050  
/ CURRENT APPLICATION NUMBER: US/09/221,236  
/ EARLIER FILING DATE: 1998-12-28  
/ EARLIER APPLICATION NUMBER: 09/163,115  
/ NUMBER OF SEQ ID NOS: 15  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 5  
/ LENGTH: 455  
/ TYPE: PR  
/ ORGANISM: Homo sapiens  
US-09-221-236-5

Alignment Scores:  
Pred. No.: 2,3e-36 Length: 455  
Score: 371.00 Matches: 81  
Percent Similarity: 56.28% Conservative: 40  
Best Local Similarity: 37.67% Mismatches: 80  
Query Match: 29.63% Indels: 14  
Gaps: 8

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-09-221-236-5 (1-455)

QY 4 GAGCTTCGGCAGTTATCCCGTGGAAACCATCTTAATTTGTAAGCTTATGAGCCTGC 63  
Db 53 GluAlaGluIleLeuSerValIleuSerHisArgAsnIleIleGlnPheTyrGlyValIle 72  
QY 64 TTGAATCCA-----GTGTCTTGTGATGATATGCTGAAGGGGGCTTTATATAT 117  
Db 73 LeuGluProProAsnTyrGlyIleValThrGluTyrAlaSerLeuGlySerLeuTyrAsp 92  
QY 118 GTGCTGCATGCT-----GCTGAACCATTTGCCATATTAATCTGCTGCCACGAATGAGT 171  
Db 93 TyrIleAsnSerAsnArgSerGluGluMet-----AspMetAspHisIleMetThr 109  
QY 172 TGGTGTTCACAGTGTCCCAAGAGAGTGGCTTATCTTACAGCATGCAACCAAGCGCTA 231  
Db 110 TrpAlaThrAspValAlaLysGlyMetHisTyrLeuHisMetGluAlaProValLysVal 129  
QY 232 ATTTCACAGGAGCTGAAACCAACCACTTAAGCTGCTGGTTCAGGGGGGACAGTTCTAAA 291  
Db 130 IleHisArgAspLeuLysSerArgAsnValIleAlaLysArgLys-----ValLeuLys 148

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QY 292 ATTGATTTGGTACAGCCTGTGACATTGACACACATGACCAATTAACAAG----- 345
DB 149 IIECyAspPheGly---AlaSerArgPheHisAsnHisThrThrHisMetSerLeuVal 167
QY 346 GGGAGTCTGCTTGGATGACCTGAAGATTGTTGAGAGTAGTAATTACAGTGAATAAATGT 405
DB 168 G1ThrPheProThrMetAlaProGluVal111LeuSerLeuProValSerGluThrCys 187
QY 406 GAGCTTTGACGCTGGGATATTATCTTTGGAGATGAATAACGCTGCGAAACCTTTGAT 465
DB 188 AspThrTyrSerTyrGlyVal1ValLeuThrGluMetLeuThrArgGluVal1ProPheLys 207
QY 466 GAGATTGTGGCCAGCTTCCGAATGATGTG---GCTGTGATAATGAGTACTGACCA 522
DB 208 GlyLeuGluGly-----LeuGlnValAla1ThrLeuVal1ValGluLysAsnGluArgLeu 225
QY 523 CCACTGATTAATAAATTATTAACCTTAAGCCATTAAGAGCTGATGACTGCTTGTGCTTAA 582
DB 226 Thr1LeuProSerSerCysProArgSerPheAlaGluLeuMetHisGlnCysTrpGluVala 245
QY 583 GATCTTCCAGCGCCTTTCATATGAGAGAAATTGTGAATAATATG 627
DB 246 AspAlaLysLysArgProSerPheLysGln1LeuSer1Leu 260
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## RESULT 11

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US-09-221-416-5
; Sequence 5, Application US/09221416
; Patent No. 6153417
; GENERAL INFORMATION:
; APPLICANT: Action, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: NMI-050
; CURRENT APPLICATION NUMBER: US/09/221,416
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-416-5
```

## Alignment Scores:

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Pred. No.: 2,3e-36 Length: 455
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
Gaps: 8
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US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-09-221-416-5 (1-455)

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QY 4 GAGCTTGGCGAGTTATCCCGTGTGACCATCTTAATTTGTAAGCTTTATGAGCCCTGC 63
DB 53 Glu1aGlu1leuSerVal1leuSerHisArgAsn1le1leGlnPheTyrGlyVal1le 72
QY 64 TTGAATCA-----GTGTGCTTGTGATGGAATAATGCTGAAGGGGCTCTTTATATAT 117
DB 73 LeuGluProProAsnTyrGly1leVal1ThrGluTyrAlaSerLeuGlySerLeuTyrAsp 92
QY 118 GTGCTGCATGAGT-----GCTGAACCATTTGCCATATTACTGCTGCCACGCAATGAGT 171
DB 93 Tyr1leAsnSerAsnArgSerGluGluMet-----AspMetAspHis1leMetThr 109
QY 172 TGGGTATTACAGTGTCCCAAGAGAGTGCTTATCTTCACAGATGCAACCCAAAGCGCTA 231
DB 110 Trp1aThrAspValAla1aLysGlyMetHisTyrLeuHisMetGluAlaProValLysVal 129
QY 232 ATTCAAGAGGAGCTGAACCAACCAAACTTACTGCTGTGAGGGGGGAGAGTCTTAATA 291
DB 130 IleHisArgAspLeuLysSerArgAsnVal1Val1leAla1aAspGly---ValLeuLys 148
```

```
QY 292 ATTGATTTGGTACAGCCTGTGACATTGACACACATGACCAATTAACAAG----- 345
DB 149 IIECyAspPheGly---AlaSerArgPheHisAsnHisThrThrHisMetSerLeuVal 167
QY 346 GGGAGTCTGCTTGGATGACCTGAAGATTGTTGAGAGTAGTAATTACAGTGAATAAATGT 405
DB 168 G1ThrPheProThrMetAlaProGluVal111LeuSerLeuProValSerGluThrCys 187
QY 406 GAGCTTTGACGCTGGGATATTATCTTTGGAGATGAATAACGCTGCGAAACCTTTGAT 465
DB 188 AspThrTyrSerTyrGlyVal1ValLeuThrGluMetLeuThrArgGluVal1ProPheLys 207
QY 466 GAGATTGTGGCCAGCTTCCGAATGATGTG---GCTGTGATAATGAGTACTGACCA 522
DB 208 GlyLeuGluGly-----LeuGlnValAla1ThrLeuVal1ValGluLysAsnGluArgLeu 225
QY 523 CCACTGATTAATAAATTATTAACCTTAAGCCATTAAGAGCTGATGACTGCTTGTGCTTAA 582
DB 226 Thr1LeuProSerSerCysProArgSerPheAlaGluLeuMetHisGlnCysTrpGluVala 245
QY 583 GATCTTCCAGCGCCTTTCATATGAGAGAAATTGTGAATAATATG 627
DB 246 AspAlaLysLysArgProSerPheLysGln1LeuSer1Leu 260
```

## RESULT 12

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US-09-221-245-5
; Sequence 5, Application US/09221245
; Patent No. 6180358
; GENERAL INFORMATION:
; APPLICANT: Action, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: NMI-050
; CURRENT APPLICATION NUMBER: US/09/221,245
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: US 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-245-5
```

## Alignment Scores:

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Pred. No.: 2,3e-36 Length: 455
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
Gaps: 8
```

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-09-221-245-5 (1-455)

```
QY 4 GAGCTTGGCGAGTTATCCCGTGTGACCATCTTAATTTGTAAGCTTTATGAGCCCTGC 63
DB 53 Glu1aGlu1leuSerVal1leuSerHisArgAsn1le1leGlnPheTyrGlyVal1le 72
QY 64 TTGAATCA-----GTGTGCTTGTGATGGAATAATGCTGAAGGGGCTCTTTATATAT 117
DB 73 LeuGluProProAsnTyrGly1leVal1ThrGluTyrAlaSerLeuGlySerLeuTyrAsp 92
QY 118 GTGCTGCATGAGT-----GCTGAACCATTTGCCATATTACTGCTGCCACGCAATGAGT 171
DB 93 Tyr1leAsnSerAsnArgSerGluGluMet-----AspMetAspHis1leMetThr 109
QY 172 TGGGTATTACAGTGTCCCAAGAGAGTGCTTATCTTCACAGATGCAACCCAAAGCGCTA 231
DB 110 Trp1aThrAspValAla1aLysGlyMetHisTyrLeuHisMetGluAlaProValLysVal 129
QY 232 ATTCAAGAGGAGCTGAACCAACCAAACTTACTGCTGTGAGGGGGGAGAGTCTTAATA 291
DB 130 IleHisArgAspLeuLysSerArgAsnVal1Val1leAla1aAspGly---ValLeuLys 148
```

```
Db 130 ILeHiaArgAspLeuLysSerArgAsnValIleAlaAlaAspGly---ValLeuLys 148
QY 292 ATTGGATTGTTGGTACAGCTGTGACATTCAGACACATGACCAATAACAAG----- 345
Db 149 ILeCyAspPheGly---AlaSerArgPheH1saSnH1eThrThiH1meSerLeuVal 167
QY 346 GGAAGTCTGCTGGATGCGACCTGAAGTTTGAAGTGAAGTGAATTAACGTGAATAAATGT 405
Db 168 G1YThrPheProThrPheAlaProGluValIleGlnSerLeuProValSerGluThrCys 187
QY 406 GACGCTTCAGCTGGGGATTAATCTTTGGAAGTGAATACCGTCGGAACCCCTTGAT 465
Db 188 AspThrTySerTyrG1yValValLeuThrGluMetLeuThrArgGluValProPheLys 207
QY 466 GAGATTGGGGCCAGCTTCGGAATCATGTGG---GCTGTCATTAATGTACTGACCA 522
Db 208 GlyLeuGluGly-----LeuGlnValAlaThrLeuValValGluLysAsnGluArgLeu 225
QY 523 CCACTGATTAATAAATTACCTTAAGCCCATTTGAGAGCTGATGACCTGTTGGTCTAAA 582
Db 226 ThrIleProSerSerCysPheArgSerPheAlaGluLeuLeuH1sgInCysTrpGluAla 245
QY 583 GATCCTCCAGCGCCCTTCATATGAGAGAAATGTGAATATATG 627
Db 246 AspAlaLysLysArgProSerPheLysGlnIleIleSerIleLeu 260
```

## RESULT 13

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US-09-163-115-5
; Sequence 5, Application US/09163115A
; Patent No. 6183962
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/163,115A
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-163-115-5
```

```
Alignment Scores:
Pred. No.: 2,3e-36 Length: 455
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
Gaps: 8
```

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-09-163-115-5 (1-455)

```
QY 4 GAGCTTCGGAGATTATCCCGTGAACATCCCTAAATATTGAAGCTTTATGAGCCTGC 63
Db 53 G1uAlaGluIleLeuSerValIleuSerH1saArgAsnIleIleGlnPheTyrGlyValIle 72
QY 64 TTGAATCCA-----GTGTGCTTGTGATGAATATGTAAGGGGGCTTTATATAT 117
Db 73 LeuGluProProAsnTyrGlyIleValIlnGluTyrAlaSerLeuGlySerLeuTyrAsp 92
QY 118 GTGCTGCATGT-----GCTGAACATTCGCATATTAATGCTGCCACGCAATGAGT 171
Db 93 TyrIleAsnSerAsnArgSerGluGluMet-----AspMetAspH1sIleMetThr 109
QY 172 TGGTGTTCACAGTTCCTCCAGAGAGGCTTATCTTCACAGATGCAACCCAAAGCGTA 231
Db 110 TrpAlaThrAspValAlaLysGlyMetH1sTyrLeuH1sMetGluAlaProValLysVal 129
QY 232 ATTCACAGGACCTGAACCAACCAATTACTGCTGTTGACAGGGGACAGTTCTTAAA 291
Db 130 ILeH1saArgAspLeuLysSerArgAsnValIleAlaAlaAspGly---ValLeuLys 148
```

```
QY 292 ATTGGATTGTTGGTACAGCTGTGACATTCAGACACATGACCAATAACAAG----- 345
Db 149 ILeCyAspPheGly---AlaSerArgPheH1saSnH1eThrThiH1meSerLeuVal 167
QY 346 GGAAGTCTGCTGGATGCGACCTGAAGTTTGAAGTGAAGTGAATTAACGTGAATAAATGT 405
Db 168 G1YThrPheProThrPheAlaProGluValIleGlnSerLeuProValSerGluThrCys 187
QY 406 GACGCTTCAGCTGGGGATTAATCTTTGGAAGTGAATACCGTCGGAACCCCTTGAT 465
Db 188 AspThrTySerTyrG1yValValLeuThrGluMetLeuThrArgGluValProPheLys 207
QY 466 GAGATTGGGGCCAGCTTCGGAATCATGTGG---GCTGTCATTAATGTACTGACCA 522
Db 208 GlyLeuGluGly-----LeuGlnValAlaThrLeuValValGluLysAsnGluArgLeu 225
QY 523 CCACTGATTAATAAATTACCTTAAGCCCATTTGAGAGCTGATGACCTGTTGGTCTAAA 582
Db 226 ThrIleProSerSerCysPheArgSerPheAlaGluLeuLeuH1sgInCysTrpGluAla 245
QY 583 GATCCTCCAGCGCCCTTCATATGAGAGAAATGTGAATATATG 627
Db 246 AspAlaLysLysArgProSerPheLysGlnIleIleSerIleLeu 260
```

## RESULT 14

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US-09-221-528-5
; Sequence 5, Application US/09221528
; Patent No. 6190874
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,528
; EARLIER FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-221-528-5
```

```
Alignment Scores:
Pred. No.: 2,3e-36 Length: 455
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
Gaps: 8
```

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-09-221-528-5 (1-455)

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QY 4 GAGCTTCGGAGATTATCCCGTGAACATCCCTAAATATTGAAGCTTTATGAGCCTGC 63
Db 53 G1uAlaGluIleLeuSerValIleuSerH1saArgAsnIleIleGlnPheTyrGlyValIle 72
QY 64 TTGAATCCA-----GTGTGCTTGTGATGAATATGTAAGGGGGCTTTATATAT 117
Db 73 LeuGluProProAsnTyrGlyIleValIlnGluTyrAlaSerLeuGlySerLeuTyrAsp 92
QY 118 GTGCTGCATGT-----GCTGAACATTCGCATATTAATGCTGCCACGCAATGAGT 171
Db 93 TyrIleAsnSerAsnArgSerGluGluMet-----AspMetAspH1sIleMetThr 109
QY 172 TGGTGTTCACAGTTCCTCCAGAGAGGCTTATCTTCACAGATGCAACCCAAAGCGTA 231
Db 110 TrpAlaThrAspValAlaLysGlyMetH1sTyrLeuH1sMetGluAlaProValLysVal 129
QY 232 ATTCACAGGACCTGAACCAACCAATTACTGCTGTTGACAGGGGACAGTTCTTAAA 291
Db 130 ILeH1saArgAspLeuLysSerArgAsnValIleAlaAlaAspGly---ValLeuLys 148
```

Db 130 ILeHisrAgpLeuLySerArgAsnValIleAlaIaAspGly---ValIleuLys 148  
QY 292 ATTGTGATTTTGGTACAGCTGTGACATTGACACACATGACCAATTAACAG----- 345  
Db 149 ILeCysAspPheGly---AlaSerArgPheHisAsnHisThrThrHisMetSerLeuVal 167  
QY 346 GGGAGTGTCTGTGATGACCTGAGATTGTTTGAAGTAGTAATTAATTCAGTGAATAAATGT 405  
Db 168 G1YThrPheProTyrMetAlaProGluValIleGlnSerLeuProValSerGluThrCys 187  
QY 406 GACCTCTTCAGCTGGGATATTATCTTTGGAGATGATTAACGCTGCGAAAACCTTTGAT 465  
Db 188 AspThrTyrsertyrGlyValValIleuTrpGluMetLeuThrArgGluValProPheLys 207  
QY 466 GAGATTGTGGCCAGCTTCCGAATCATGTGG---GCTGTCATTAATGTACTGACCA 522  
Db 208 G1YLeuGluGly-----LeuGlnValAlaTrpLeuValValGluLysAsnGluArgLeu 225  
QY 523 CCACTGATMAAATAATTACCTTAAGCCATTGAGAGCCGATGACCTGTTGTGCTAAA 582  
Db 226 ThrIleProSerSerCysProArgSerPheAlaGluLeuLysGlnCysTrpGluAla 245  
QY 583 GATCCTTCCAGCGCCCTTCAATGAGGAAATTTGGAATAATATATG 627  
Db 246 AspAlaLysIlyArgProSerPheLysGlnIleIleSerIleLeu 260

RESULT 15  
US-09-593-553-5  
Sequence 5, Application US/09593553  
Patent No. 6200770  
GENERAL INFORMATION:  
APPLICANT: Acton, Susan  
TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
FILE REFERENCE: NMI-050  
CURRENT APPLICATION NUMBER: US/09/593,553  
CURRENT FILING DATE: 2000-06-14  
PRIOR APPLICATION NUMBER: 09/163,115  
PRIOR FILING DATE: 1998-09-28  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 5  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-593-553-5

Alignment Scores:  
Pred. No.: 2,3e-36 Length: 455  
Score: 371.00 Matches: 81  
Percent Similarity: 56.28% Conservative: 40  
Best Local Similarity: 37.67% Mismatches: 80  
Query Match: 29.63% Indels: 14  
DB: 3 Gaps: 8

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-09-593-553-5 (1-455)

QY 4 GAGCTTTCGAGATTATCCGATGTAACCACTTAATTTGTAAGCTTATGAGCCTGC 63  
Db 53 GluAlaGluIleLeuSerValIleSerHisArgAsnIleIleGlnPheTyrglyValIle 72  
QY 64 TTGAATCCA-----GTGTGCTTGTGATGAAATATGCTGAAGGGGCTTTATATATAT 117  
Db 73 LeuGluProProAsnTyrglyIleValIThrGluTyralaSerLeuGlySerLeuTyxAsp 92  
QY 118 GTGCTGACATGCT-----GCTGACCATTCATTAATTAATGCTGCGCCAGCAATGAGT 171  
Db 93 TyrIleAsnSerAsnArgSerGluGluMet-----AspMetAspHisIleMetThr 109  
QY 172 TGGTGTTTTACAGTGTTCACAGAGTGGCTTATTTTCACAGCATGCAACCAAGCGCTA 231  
Db 110 TrpAlaThrAspValAlaLysGlyMetHisTyrlleuHisMetGluAlaProValLysVal 129  
QY 232 ATTCAAGGAGCTTGAACCAACCAAACTTAATGCTGCTGTTGCAAGGGGAGCAGTTCTAAA 291

Db 130 ILeHisrAgpLeuLySerArgAsnValIleAlaIaAspGly---ValIleuLys 148  
QY 292 ATTGTGATTTTGGTACAGCTGTGACATTGACACACATGACCAATTAACAG----- 345  
Db 149 ILeCysAspPheGly---AlaSerArgPheHisAsnHisThrThrHisMetSerLeuVal 167  
QY 346 GGGAGTGTCTGTGATGACCTGAGATTGTTTGAAGTAGTAATTAATTCAGTGAATAAATGT 405  
Db 168 G1YThrPheProTyrMetAlaProGluValIleGlnSerLeuProValSerGluThrCys 187  
QY 406 GACCTCTTCAGCTGGGATATTATCTTTGGAGATGATTAACGCTGCGAAAACCTTTGAT 465  
Db 188 AspThrTyrsertyrGlyValValIleuTrpGluMetLeuThrArgGluValProPheLys 207  
QY 466 GAGATTGTGGCCAGCTTCCGAATCATGTGG---GCTGTCATTAATGTACTGACCA 522  
Db 208 G1YLeuGluGly-----LeuGlnValAlaTrpLeuValValGluLysAsnGluArgLeu 225  
QY 523 CCACTGATMAAATAATTACCTTAAGCCATTGAGAGCCGATGACCTGTTGTGCTAAA 582  
Db 226 ThrIleProSerSerCysProArgSerPheAlaGluLeuLysGlnCysTrpGluAla 245  
QY 583 GATCCTTCCAGCGCCCTTCAATGAGGAAATTTGGAATAATATATG 627  
Db 246 AspAlaLysIlyArgProSerPheLysGlnIleIleSerIleLeu 260

Search completed: August 2, 2005, 20:16:32  
Job time : 28.3378 secs



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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 2, 2005, 19:59:50 ; Search time 84.7297 Seconds

(without alignments)  
6290.398 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5  
Rgapop 6.0 , Rgapext 7.0  
Dgapop 6.0 , Dgapext 7.0

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 3490280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-O=/cgn2\_1/USPRO spool/US09830144/runat\_02082005\_101033\_11881/app\_query.faeta\_1.1230  
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-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1252	100.0	336	Sequence 135, App
2	1252	100.0	518	Sequence 2, Appl
3	1252	100.0	518	Sequence 13, Appl
4	1252	100.0	579	Sequence 4, Appl
5	1252	100.0	579	Sequence 4, Appl
6	1252	100.0	590	Sequence 15, Appl
7	1252	100.0	590	Sequence 15, Appl
8	1233.5	98.5	623	Sequence 13442, A
9	1221	97.5	616	Sequence 13629, A
10	1215	97.0	615	Sequence 13628, A
11	815	65.1	268	Sequence 13508, A
12	392.5	31.3	330	Sequence 136, App
13	392.5	31.3	953	Sequence 56, Appl
14	392.5	31.3	953	Sequence 98, Appl
15	392.5	31.3	954	Sequence 97, Appl
16	392.5	31.3	954	Sequence 187, App
17	387.5	31.0	940	Sequence 223, App
18	387.5	31.0	1018	Sequence 13436, A
19	379	30.3	422	Sequence 132604, A
20	377	30.1	376	Sequence 173612, A
21	376	30.0	371	Sequence 13608, A
22	374.5	29.9	376	Sequence 271998, A
23	374.5	29.9	2964	Sequence 13552, A
24	373.5	29.8	603	Sequence 155923, A
25	373	29.8	357	Sequence 352964, A
26	373	29.8	415	Sequence 351552, A
27	373	29.8	432	Sequence 607936, A
28	373	29.8	433	Sequence 57936, A
29	372	29.7	289	Sequence 13427, A
30	372	29.7	415	Sequence 351548, A
31	372	29.7	426	Sequence 55173, A
32	372	29.7	426	Sequence 58969, A
33	372	29.7	454	Sequence 13429, A
34	372	29.7	802	Sequence 13428, A
35	371	29.6	312	Sequence 137, App
36	371	29.6	349	Sequence 6345, Ap
37	371	29.6	417	Sequence 46882, A
38	371	29.6	455	Sequence 5, Appl
39	371	29.6	455	Sequence 2477, Ap
40	371	29.6	455	Sequence 2, Appl
41	371	29.6	455	Sequence 5, Appl
42	371	29.6	473	Sequence 837, App
43	371	29.6	800	Sequence 1101, Ap
44	371	29.6	800	Sequence 66, Appl
45	371	29.6	800	Sequence 64, Appl

## ALIGNMENTS

RESULT 1  
US-10-664-421-135  
Sequence 135, Application US/10664421  
Publication No. US20040142864A1  
GENERAL INFORMATION:  
APPLICANT: BREMER, RYAN  
APPLICANT: IBRAHIM, PRABHA  
APPLICANT: KIMAR, ABHINAV  
APPLICANT: MANDIYAN, VALSAN  
APPLICANT: MILBURN, MICHAEL V.  
TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE  
FILE REFERENCE: 039363/0703  
CURRENT APPLICATION NUMBER: US/10/664,421  
CURRENT FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: 60/412,341  
PRIOR FILING DATE: 2002-09-20  
PRIOR APPLICATION NUMBER: 60/411,398  
PRIOR FILING DATE: 2002-09-16  
NUMBER OF SEQ ID NOS: 169  
SOFTWARE: PatentIn Ver. 3.2

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; SEQ ID NO 135
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-135

Alignment Scores:
Pred. No.: 2, 81e-128
Score: 1252.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Matches: 336
Conservative: 228
Mismatches: 0
Indels: 0
Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x US-10-664-421-135 (1-336)

QY 1 GTAGAGCTTCGGCAGTTATCCGCTGTGAACCATCTTAATTTGTAACCTTTATGAGCC 60
Db ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIleLeuTyrGlyAla 95
QY 61 TGCCTGAATCCAGTGTCTTGATGGAATATGCTGAAGGGGCTCTTATATATATG 120
Db CysLeuAsnProValCysLeuValMetGlnTyrAlaGlnGlySerLeuTyrAsnVal 115
QY 121 CTGATGTGTCTGAACCATTCGATATTAATCTGCTGCCACGCAATGATGTGTTA 180
Db LeuHisGlyAlaGlnProLeuProTyrThrAlaAlaHisAlaMetSerTyrCysLeu 135
QY 181 CAGGTTCGCCAAGAGTGGCTTATCTTACAGCATGCAACCCAAAGGCTTATTCACAG 240
Db GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProValAlaLeuIleHisArg 155
QY 241 GACCTGAACCAACAACCTTACTGCTGTGTCAGGGGGACAGTTCTTAAATTTGAT 300
Db AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValIleLeuLysIleCysAsp 175
QY 301 TTTGGTACAGCTGTGATTCAGACACACATGACCAATTAACAAGGAGTGTGCTGG 360
Db PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 195
QY 361 ATGGCAGCTGAAGTTTGAAGGTAATTAACGTGAAAAATGTGACGTTCCAGCTGG 420
Db MetAlaProGlnValIlePheGlnGlySerAsnLysSerIleLysCysAspValPheSerTyr 215
QY 421 GGTATTATTTTGGGAAGTATACCGCTCGAAGAACCTTTGATGAGATGTGGCCCA 480
Db GlyIleIleLeuTyrGlnValIleThrArgArgLysProPheAspGlnIleGlyPro 235
QY 481 GCTTCCGAATCAGTGGGCTGTTCATATGTAATGTAAGTACCAACCACTGATAAAAATTA 540
Db GlnTyrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 525
QY 541 CTTAAGCCATTGAGAGCTGATGACTCGTTGTGCTTAAAGATCTTCCAGCCGCT 600
Db ProLysProIleGlnSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 275
QY 601 TCAATGAGGAATTTGAAAATTAATGACTCACTTATGCGGTACTTTCCAGAGCAGAT 660
Db 276 SerMetGlnGlnIleValIleValIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
QY 661 GAGCATTACAGATCCTTGTGAG 684
Db 296 GlnProLeuGlnIleTyrProCysGln 303

RESULT 2
US-10-283-023-2
; Sequence 2, Application US/10283023
; Publication No. US20030091573A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: Methods and compositions for the
; diagnosis and treatment of hematological disorders using
; TITLE OF INVENTION: 16319
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; FILE REFERENCE: WP101-239P1RM
; CURRENT APPLICATION NUMBER: US/10/283,023
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-283-023-2

Alignment Scores:
Pred. No.: 3, 14e-128
Score: 1252.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Matches: 518
Conservative: 228
Mismatches: 0
Indels: 0
Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x US-10-283-023-2 (1-518)

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QY 121 CTGATGTGTCTGAACCATTCGATATTAATCTGCTGCCACGCAATGATGTGTTA 180
Db LeuHisGlyAlaGlnProLeuProTyrThrAlaAlaHisAlaMetSerTyrCysLeu 135
QY 181 CAGGTTCGCCAAGAGTGGCTTATCTTACAGCATGCAACCCAAAGGCTTATTCACAG 240
Db GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProValAlaLeuIleHisArg 155
QY 241 GACCTGAACCAACAACCTTACTGCTGTGTCAGGGGGACAGTTCTTAAATTTGAT 300
Db AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValIleLeuLysIleCysAsp 175
QY 301 TTTGGTACAGCTGTGATTCAGACACACATGACCAATTAACAAGGAGTGTGCTGG 360
Db PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 195
QY 361 ATGGCAGCTGAAGTTTGAAGGTAATTAACGTGAAAAATGTGACGTTCCAGCTGG 420
Db MetAlaProGlnValIlePheGlnGlySerAsnLysSerIleLysCysAspValPheSerTyr 215
QY 421 GGTATTATTTTGGGAAGTATACCGCTCGAAGAACCTTTGATGAGATGTGGCCCA 480
Db GlyIleIleLeuTyrGlnValIleThrArgArgLysProPheAspGlnIleGlyPro 235
QY 481 GCTTCCGAATCAGTGGGCTGTTCATATGTAATGTAAGTACCAACCACTGATAAAAATTA 540
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Db 276 SerMetGlnGlnIleValIleValIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
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Db 296 GlnProLeuGlnIleTyrProCysGln 303

RESULT 3
US-10-386-414-13
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Sequence 13, Application US/10386414
Publication No. US2004006016A1
GENERAL INFORMATION:
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Robison, Keith E.
APPLICANT: White, David
APPLICANT: Williamson, Mark W.
APPLICANT: Cook, William James
APPLICANT: Meyers, Rachel E.
APPLICANT: MacBeth, Kyle J.
APPLICANT: Carroll, Joseph M.
APPLICANT: Chun, Miyoung
TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
FILE REFERENCE: MET03-0210NMIM
CURRENT APPLICATION NUMBER: US/10/386,414
PRIOR FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: 09/426,282
PRIOR FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 09/668,266
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/330,970
PRIOR FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: 09/724,599
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/860,193
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 10/283,023
PRIOR FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 60/335,044
PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 10/010,943
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/254,037
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 09/833,082
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 518
TYPE: PRT
ORGANISM: Homo Sapien
US-10-386-414-13

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Pred. No.: 3,14e-128 Length: 518
Score: 1252.00 Matches: 228
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 15

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QY 61 TGCCTTGAATCCAGTGTCTCTTGTATGTAATGTAATGTAAGGGGCTCTTTATTAATG 120
DB 96 CysLeuAsnProValCysLeuValMetGlnTyrAlaGlnGlyGlySerLeuTyrAsnVal 115
QY 121 CTGATGCTGTGTAACCATTCATATTAATCTGCTGCCACGCAATGAGTTGTGTTTA 180
DB 116 LeuHisGlyAlaGlnProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 135
QY 181 CAGTGTCCCAAGAGTGGCTTATCTTCAACAGATGCAACCAAGCGCTTAATTACAGG 240
DB 136 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProTyrAlaLeuIleHisArg 155
QY 241 GACCGAAGCAACCAACTCTGCTGTTGCAAGGGGAGCAAGTCTTAATAATTGTGAT 300
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DB 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnHisLysGlySerAlaIleTyr 195
QY 361 ATGGACCTGGAAGTTTGAAGGTAGTAATTACAGTGAAGAAATGTGACGCTTCAGCTGG 420
DB 196 MetAlaProGlnValPheGlnGlySerAsnTyrSerGlnLysCysAspValPheSerTyr 215
QY 421 GGTATTAATCTTTGGGAAGTATGATTAACCGCTGGAAACCTTTATGATGATGGCCCA 480
DB 216 GlyIleIleLeuTyrGlnValIleThrArgAlaGlyProPheAspGlnIleGlyGlyPro 235
QY 481 GCTTCCGATCATGTGGGCTGTTCAATATGTAATGTAATGTAATGTAATGTAATGTAAT 540
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QY 661 GAGCCATTACAGTATCTTGTCCAG 684
DB 296 GluProLeuGlnTyrProCysGln 303

RESULT 4
US-10-158-895-4
Sequence 4, Application US/10158895
Publication No. US20020155624A1
GENERAL INFORMATION:
APPLICANT: ONO, KOICHIRO
APPLICANT: OHTOMO, TOSHIHIKO
APPLICANT: TSUCHIYA, MASAYUKI
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
FILE REFERENCE: 053466/0278
CURRENT APPLICATION NUMBER: US/10/158,895
PRIOR FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US/09/529,279
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: PCT/JP98/04796
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: JP 9/290188
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-10-158-895-4

Alignment Scores:
Pred. No.: 3,23e-128 Length: 579
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 13

US-09-830-144-1_COPY_408_1091 (1-684) x US-10-158-895-4 (1-579)
QY 1 GTAGAGCTTGGGAGATTATCCGTTGTAACCATCTTAATTTGTAAGCTTTATGAGCC 60
DB 76 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValylLeuTyrClyAla 95
QY 61 TGCCTTGAATCCAGTGTCTCTTGTATGTAATGTAATGTAAGGGGCTCTTTATTAATG 120
DB 96 CysLeuAsnProValCysLeuValMetGlnTyrAlaGlnGlyGlySerLeuTyrAsnVal 115
```

QY 121 CTGCATGCTGTCGAACCATTCGCTTACTGCTGCCACGCAATGAGTGTGTTTA 180  
DB 116 LeuHISGLYALAGLIPROLEUPROTYRTRHRLAALAHLEMESETTRIPYSALEU 135  
QY 181 CAGTGTCCCAAGAGTGGCTTATCTTCACACATGCAACCCAAAGCCCTTAATTCACAGG 240  
DB 136 GlnCYSSERGLNGLYVALALATYRLEUHSERMETGlnPROLYSALALeuILeHISArg 155  
QY 241 GACCTGAAACCAACCAACTTACTGCTGTGTGTCAGGGGAGACAGTCTTAAAAATTTGTGAT 300  
DB 156 AspleuLYSProProAsnleuLeuValAlaGLYGLYTHrValLeuLYSLeCYsAsp 175  
QY 301 TTGGTACAGCCTGTGACATTCAGACACATGACCAATAACAGGGAGTGTGCTTGG 360  
DB 176 PheGLYTHrAlACYSAspILeGLNTHrHISMETThrAsnleuLYSGLYSERAlaAlaTrp 195  
QY 361 ATGGCACTGGAAGTTTGAAGGTAGTAATTACAGTGAATAATGACGTCTTCAGCTGG 420  
DB 196 MetAlaProGLUValPheGLUGLYSERAsnTYRserGLULYSCYsAspValPheSerTrp 215  
QY 421 GGTATTATCTTTGGGAAGTGAACGCGTCGGAACCCCTTGAATGAGATTGTGCGCCA 480  
DB 216 GlyIleIleLeuTRPGLUValILeThrArgArgLYSProPheAspGLUILeGLYGLYPro 235  
QY 481 GCTTCCGATCATGTCGGCTGTTCATTAATGTACTGACACACATGATTAATAATTTA 540  
DB 236 AlaPheArgIleMETTRPAlaValHISAsnGLYTHrArgProPheLeuILeLYSAsnLeu 255  
QY 541 CCTAAGCCCATTTGAGAGCCTGATGACTGTGTGTGCTTAAAGATCCCTCCAGCGCCT 600  
DB 256 ProLYSProILeGLUserLeuMETThrArgCYsTrpserLYSAspProSerGLINArgPro 275  
QY 601 TCATGAGAGAAATTTGGAATAATATGACTCACTTGAATGCGGTACTTTCCAGAGCAGAT 660  
DB 276 SerMetGLUGLUILeValLYSILeMETThrHISleuMetArgTYRPhEProGLYAlaAsp 295  
QY 661 GAGCCATTACAGTATCCCTTGCAG 684  
DB 296 GluProLeuGLNTRYProCYsGLN 303

RESULT 5  
US-10-384-743-4  
; Sequence 4, Application US/10384743  
; Publication No. US20030162228A1  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHITAKO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/10/384,743  
; PRIOR FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: US/09/529,279  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: JP 9/290188  
; PRIOR FILING DATE: 1997-10-22  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-384-743-4

Alignment Scores:  
Pred. No.: 3,23e-128 Length: 579  
Score: 1252.00 Matches: 228  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0

DB: 14 Gaps: 0  
US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-10-384-743-4 (1-579)  
QY 1 GTAGAGCTTGGGAGATTATCCGTGTGAACCATCTTAATTTGTAAGCTTTATGAGGCC 60  
DB 76 ValGLIleuValArgILeUSeRArgValAsnHISProAsnILeValLYSLeuTYRGLYAla 95  
QY 61 TGGCTGAATTCAGTGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTATTAATATGTG 120  
DB 96 CYLeuAsnProValCYsLeuValMetGLUTYRAlaGLUGLYGLYserLeuTYRAsnVal 115  
QY 121 CTGCATGCTGTCGAACCATTCGCTTACTGCTGCCACGCAATGAGTGTGTTTA 180  
DB 116 LeuHISGLYALAGLIPROLEUPROTYRTRHRLAALAHLEMESETTRIPYSALEU 135  
QY 181 CAGTGTCCCAAGAGTGGCTTATCTTCACACATGCAACCCAAAGCCCTTAATTCACAGG 240  
DB 136 GlnCYSSERGLNGLYVALALATYRLEUHSERMETGlnPROLYSALALeuILeHISArg 155  
QY 241 GACCTGAAACCAACCAACTTACTGCTGTGTGTCAGGGGAGACAGTCTTAAAAATTTGTGAT 300  
DB 156 AspleuLYSProProAsnleuLeuValAlaGLYGLYTHrValLeuLYSLeCYsAsp 175  
QY 301 TTGGTACAGCCTGTGACATTCAGACACATGACCAATAACAGGGAGTGTGCTTGG 360  
DB 176 PheGLYTHrAlACYSAspILeGLNTHrHISMETThrAsnleuLYSGLYSERAlaAlaTrp 195  
QY 361 ATGGCACTGGAAGTTTGAAGGTAGTAATTACAGTGAATAATGACGTCTTCAGCTGG 420  
DB 196 MetAlaProGLUValPheGLUGLYSERAsnTYRserGLULYSCYsAspValPheSerTrp 215  
QY 421 GGTATTATCTTTGGGAAGTGAACGCGTCGGAACCCCTTGAATGAGATTGTGCGCCA 480  
DB 216 GlyIleIleLeuTRPGLUValILeThrArgArgLYSProPheAspGLUILeGLYGLYPro 235  
QY 481 GCTTCCGATCATGTCGGCTGTTCATTAATGTACTGACACACATGATTAATAATTTA 540  
DB 236 AlaPheArgIleMETTRPAlaValHISAsnGLYTHrArgProPheLeuILeLYSAsnLeu 255  
QY 541 CCTAAGCCCATTTGAGAGCCTGATGACTGTGTGTGCTTAAAGATCCCTCCAGCGCCT 600  
DB 256 ProLYSProILeGLUserLeuMETThrArgCYsTrpserLYSAspProSerGLINArgPro 275  
QY 601 TCATGAGAGAAATTTGGAATAATATGACTCACTTGAATGCGGTACTTTCCAGAGCAGAT 660  
DB 276 SerMetGLUGLUILeValLYSILeMETThrHISleuMetArgTYRPhEProGLYAlaAsp 295  
QY 661 GAGCCATTACAGTATCCCTTGCAG 684  
DB 296 GluProLeuGLNTRYProCYsGLN 303

RESULT 6  
US-10-158-895-15  
; Sequence 15, Application US/10158895  
; Publication No. US20020155624A1  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHITAKO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/10/158,895  
; PRIOR FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: US/09/529,279  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: JP 9/290188  
; PRIOR FILING DATE: 1997-10-22  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15

LENGTH: 590  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-15

## Alignment Scores:

Pred. No.:	3,256-128	Length:	590
Score:	1252.00	Matches:	228
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-10-158-895-15 (1-590)

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OY 1 GTAGAGCTTCGGCAGTTATCCGTTGAGAACCATCTTAATATTGTAAGCTTTATGAGACC 60
DB ValGluLeuArGlnLeuSerArgValAsnHisProAsnIleValIysLeuTrpGlyAla 95
OY 61 TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATATATG 120
DB CysLeuAsnProValCysLeuValMetGluTrpAlaGluGlySerLeuTrpAsnVal 115
OY 121 CTGATGATGCTGGAACCATTCATATATCTGCTGCCACGCAATGATGGTGTTA 180
DB LeuHisGlyAlaGluProLeuProTyrTrpAlaHisAlaMetSerTrpCysLeu 135
OY 116 LeuHisGlyAlaGluProLeuProTyrTrpAlaHisAlaMetSerTrpCysLeu 135
OY 181 CAGTGTTCCTCCAGAGAGTGGCTTATCTTCACAGATGCAACCAAGCGCTAATTCACAG 240
DB GlnCysSerGlnGlyValAlaIleTrpLeuHisSerMetGlnProIysAlaLeuIleHisArg 155
OY 136 GlnCysSerGlnGlyValAlaIleTrpLeuHisSerMetGlnProIysAlaLeuIleHisArg 155
OY 241 GACCTGAAACCAACCAACTTACTGCTGTGATGAGGGGGGACAGTTCTTAAATTTGTGAT 300
DB AspLeuAsnProValCysLeuValMetGluTrpAlaGluGlySerLeuTrpAsnVal 115
OY 156 AspLeuAsnProValCysLeuValMetGluTrpAlaGluGlySerLeuTrpAsnVal 115
OY 301 TTTGGTACAGCTGTGATTCACAGACACATGACCAATTAACAAGGGAGTGGCTGG 360
DB PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 195
OY 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 195
OY 361 ATGGCACTGGAAGTTTGAAGGTATTAATTAACAGTGAATAATGATGAGCTTCAGCTGG 420
DB MetAlaProGluValPheGluGlySerAsnTrpSerGluLysCysAspValPheSerTrp 215
OY 196 MetAlaProGluValPheGluGlySerAsnTrpSerGluLysCysAspValPheSerTrp 215
OY 421 GGTATTTATCTTTGGGAAGTATTAACGCGTCGGAACCTTTGATGATGATGGTGCCCA 480
DB GlyIleIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 235
OY 216 GlyIleIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 235
OY 481 GCTTTCCGAATCATGTGGGCTGTTCAATAGTACTGACCAACCACTGATTAATAATTTA 540
DB GCTTTCCGAATCATGTGGGCTGTTCAATAGTACTGACCAACCACTGATTAATAATTTA 540
OY 236 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 255
OY 541 CTTAAGCCCATTTGAGAGCTGATGACTGTTGTTGGTCTTAAAGATCTTCCAGAGGCCCT 600
DB ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 275
OY 256 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 275
OY 601 TCAATGAGAGAATTTGTAATAATTAATGACTCACTTATGATGCGTACTTTCCAGAGCAAT 660
DB TCAATGAGAGAATTTGTAATAATTAATGACTCACTTATGATGCGTACTTTCCAGAGCAAT 660
OY 276 SerMetGluGluIleValIysIleMetThrHisLeuMetArgTrpPheProGlyAlaAsp 295
DB SerMetGluGluIleValIysIleMetThrHisLeuMetArgTrpPheProGlyAlaAsp 295
OY 661 GAGCCATTACAGTATCTTGTTCAG 684
DB GAGCCATTACAGTATCTTGTTCAG 684
OY 296 GluProLeuGlnTrpProCysGln 303
DB GluProLeuGlnTrpProCysGln 303
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## RESULT 7

US-10-384-743-15  
Sequence 15, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAHIKU  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278

CURRENT APPLICATION NUMBER: US/10/384,743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 590  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-384-743-15

## Alignment Scores:

Pred. No.:	3,256-128	Length:	590
Score:	1252.00	Matches:	228
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-10-384-743-15 (1-590)

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OY 1 GTAGAGCTTCGGCAGTTATCCGTTGAGAACCATCTTAATATTGTAAGCTTTATGAGACC 60
DB ValGluLeuArGlnLeuSerArgValAsnHisProAsnIleValIysLeuTrpGlyAla 95
OY 61 TGCTTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATATATG 120
DB CysLeuAsnProValCysLeuValMetGluTrpAlaGluGlySerLeuTrpAsnVal 115
OY 96 CysLeuAsnProValCysLeuValMetGluTrpAlaGluGlySerLeuTrpAsnVal 115
OY 121 CTGATGATGCTGGAACCATTCATATATCTGCTGCCACGCAATGATGGTGTTA 180
DB LeuHisGlyAlaGluProLeuProTyrTrpAlaHisAlaMetSerTrpCysLeu 135
OY 116 LeuHisGlyAlaGluProLeuProTyrTrpAlaHisAlaMetSerTrpCysLeu 135
OY 181 CAGTGTTCCTCCAGAGAGTGGCTTATCTTCACAGATGCAACCAAGCGCTAATTCACAG 240
DB GlnCysSerGlnGlyValAlaIleTrpLeuHisSerMetGlnProIysAlaLeuIleHisArg 155
OY 136 GlnCysSerGlnGlyValAlaIleTrpLeuHisSerMetGlnProIysAlaLeuIleHisArg 155
OY 241 GACCTGAAACCAACCAACTTACTGCTGTGATGAGGGGGGACAGTTCTTAAATTTGTGAT 300
DB AspLeuAsnProValCysLeuValMetGluTrpAlaGluGlySerLeuTrpAsnVal 115
OY 156 AspLeuAsnProValCysLeuValMetGluTrpAlaGluGlySerLeuTrpAsnVal 115
OY 301 TTTGGTACAGCTGTGATTCACAGACACATGACCAATTAACAAGGGAGTGGCTGG 360
DB PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 195
OY 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 195
OY 361 ATGGCACTGGAAGTTTGAAGGTATTAATTAACAGTGAATAATGATGAGCTTCAGCTGG 420
DB MetAlaProGluValPheGluGlySerAsnTrpSerGluLysCysAspValPheSerTrp 215
OY 196 MetAlaProGluValPheGluGlySerAsnTrpSerGluLysCysAspValPheSerTrp 215
OY 421 GGTATTTATCTTTGGGAAGTATTAACGCGTCGGAACCTTTGATGATGATGGTGCCCA 480
DB GlyIleIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 235
OY 216 GlyIleIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 235
OY 481 GCTTTCCGAATCATGTGGGCTGTTCAATAGTACTGACCAACCACTGATTAATAATTTA 540
DB GCTTTCCGAATCATGTGGGCTGTTCAATAGTACTGACCAACCACTGATTAATAATTTA 540
OY 236 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 255
OY 541 CTTAAGCCCATTTGAGAGCTGATGACTGTTGTTGGTCTTAAAGATCTTCCAGAGGCCCT 600
DB ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 275
OY 256 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 275
OY 601 TCAATGAGAGAATTTGTAATAATTAATGACTCACTTATGATGCGTACTTTCCAGAGCAAT 660
DB TCAATGAGAGAATTTGTAATAATTAATGACTCACTTATGATGCGTACTTTCCAGAGCAAT 660
OY 276 SerMetGluGluIleValIysIleMetThrHisLeuMetArgTrpPheProGlyAlaAsp 295
DB SerMetGluGluIleValIysIleMetThrHisLeuMetArgTrpPheProGlyAlaAsp 295
OY 661 GAGCCATTACAGTATCTTGTTCAG 684
DB GAGCCATTACAGTATCTTGTTCAG 684
OY 296 GluProLeuGlnTrpProCysGln 303
DB GluProLeuGlnTrpProCysGln 303
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RESULT 8  
US-10-732-923-13442  
; Sequence 13442, Application US/10732923  
; Publication No. US20050108791A1  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923  
; PRIOR FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154  
; PRIORITY DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO 13442  
; LENGTH: 623  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-732-923-13442

Alignment Scores:  
Pred. No.: 3,566-126 Length: 623  
Score: 1233.50 Matches: 228  
Percent Similarity: 93.06% Conservative: 0  
Best Local Similarity: 93.06% Mismatches: 0  
Query Match: 98.52% Indels: 17  
DB: 17 Gaps: 1

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-10-732-923-13442 (1-623)

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QY 1 GTAGAGCTTCGGAGATTATCCGCTGTGAACCATCTTAATATGTAAGCTTTATGAGCC 60
DB 76 ValGluLeuAArgGlnLeuSerAArgValAsnHisProAsnIleValIlySLeuYrGlyAla 95
QY 61 TGCCTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTATATATATG 120
DB 96 CysLeuAsnProValCysLeuValMetGluTrpAlaGluGlySerLeuYrAsnVal 115
QY 121 CTGATGAGTGTGTAACCATTCATTTATATGCTGCTGCCAAGCAAGATTTGGTTT 180
DB 116 LeuHisGlyAlaGluTrpLeuProYrTrpThrAlaAlaHisAlaMetSerTrpCysLeu 135
QY 181 CAGTGTTCCTCAAGAGTGGCTTATCTTACAGCATGCAACCAAGGGCTTAATTCACAG 240
DB 136 GlnCysSerGlnGlyValAlaTrpLeuHisSerMetGlnProIlySalLeuIleHisArg 155
QY 241 GACCTGAACCAACCAACTTACTGCTGTGTCAGGGGGACAGTTCTAAAATTTGTGAT 300
DB 156 AspLeuAsnProValCysLeuValMetGluTrpAlaGlyGlyThrValLeuYrIleCysAsp 175
QY 301 TTGTGTACAGCTGTGATTCATTCAGACACATGACCAATTAAGGGAGTGTGCTGG 360
DB 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnYrGlySerAlaAlaTrp 195
QY 361 ATGGCACCCTGAAGTTTGTGAAGTATTAATTAAGTAAATATGACGCTTCACCTGG 420
DB 196 MetAlaProGluValPheGlnGlySerAsnYrSerGluIlyCysAspValPheSerTrp 215
QY 421 GGTATTTATCTTTGGGAGATGATACGCGTGGAAACCTTTGATAGATTTGGTGGCCA 480
DB 216 GlyIleIleLeuTrpGluValIleThrArgArgValPheProIlyGlyGlyPro 235
QY 481 GCTTTCCGAATCATGTGGGCTGTTCATTAATGTAATGTAATGTAATGTAATGTAAT 540
DB 236 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProIlyLeuIleHisAsnLeu 255
QY 541 CCTAAGCCATTTGAGAGCTGATGATCTGTTGTGTCTTAAGATCTTCCAGGGCCCT 600
DB 256 ProIlySerProIleIleLeuSerLeuMetThrArgCysTrpSerIlyAspProSerGlnArgPro 275
QY 601 TCAATGAGAAATGTTGAAAATTAATGACTCACTGATGCGG----- 642
DB 276 SerMetGluGluIleValIlySerIleMetThrHisLeuMetArgGlyLeuLeuCysThrGlu 295
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QY 643 -----TACTTCCAGAGACAGATGAGCCATTA 669
DB 296 GlyIleLeuAsnArgAspLeuLeuLeuGlnIlyPheProGlyAlaAspGluProLeu 315
QY 670 CAGTATCCCTGTGAG 684
DB 316 GlnIlyProCysGln 320
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RESULT 9  
US-10-732-923-13629  
; Sequence 13629, Application US/10732923  
; Publication No. US20050108791A1  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923  
; PRIOR FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154  
; PRIORITY DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO 13629  
; LENGTH: 616  
; TYPE: PRT  
; ORGANISM: Xenopus laevis  
US-10-732-923-13629

Alignment Scores:  
Pred. No.: 8,396-125 Length: 616  
Score: 1221.00 Matches: 222  
Percent Similarity: 98.68% Conservative: 3  
Best Local Similarity: 97.37% Mismatches: 3  
Query Match: 97.52% Indels: 0  
DB: 17 Gaps: 0

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-10-732-923-13629 (1-616)

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QY 1 GTAGAGCTTCGGAGATTATCCGCTGTGAACCATCTTAATATGTAAGCTTTATGAGCC 60
DB 65 ValGluLeuAArgGlnLeuSerAArgValAsnHisProAsnIleValIlySLeuYrGlyAla 84
QY 61 TGCCTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTATATATATG 120
DB 85 CysLeuAsnProValCysLeuValMetGluTrpAlaGluGlySerLeuYrAsnVal 104
QY 121 CTGATGAGTGTGTAACCATTCATTTATATGCTGCTGCCAAGCAAGATTTGGTTT 180
DB 105 LeuHisGlyAlaGluTrpLeuProYrTrpThrAlaAlaHisAlaMetSerTrpCysLeu 124
QY 181 CAGTGTTCCTCAAGAGTGGCTTATCTTACAGCATGCAACCAAGGGCTTAATTCACAG 240
DB 125 GlnCysAlaGlnGlyValAlaTrpLeuHisSerMetLeuProIlySalLeuIleHisArg 144
QY 241 GACCTGAACCAACCAACTTACTGCTGTGTCAGGGGGACAGTTCTAAAATTTGTGAT 300
DB 145 AspLeuAsnProValCysLeuValMetGluTrpAlaGlyGlyThrValLeuYrIleCysAsp 164
QY 301 TTGTGTACAGCTGTGATTCATTCAGACACATGACCAATTAAGGGAGTGTGCTGG 360
DB 165 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnYrGlySerAlaAlaTrp 184
QY 361 ATGGCACCCTGAAGTTTGTGAAGTATTAATTAAGTAAATATGACGCTTCACCTGG 420
DB 185 MetAlaProGluValPheGlnGlySerAsnYrSerGluIlyCysAspValPheSerTrp 204
QY 421 GGTATTTATCTTTGGGAGATGATACGCGTGGAAACCTTTGATAGATTTGGTGGCCA 480
DB 205 GlyIleIleLeuTrpGluValIleThrArgArgValPheProIlyGlyGlyPro 224
QY 481 GCTTTCCGAATCATGTGGGCTGTTCATTAATGTAATGTAATGTAATGTAATGTAAT 540
DB 225 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProIlyLeuIleHisAsnLeu 244
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QY      541  CCGAAGCCCATTTGAGAGCGCTAGTACTGTTGTGTCTTAAAGAACTTCCAGAGCCCT 600
Db      245  PPLysProlleGInserLeuMetCtnrAtGcYsttPseLysAspProGlnrPro 264
QY      601  TCAATGAGGAAATTTGTGAAATAATAGTACTTGATGCGGTACTTTCAGAGCAGAT 666
Db      265  SerMetClnGlnLeuValLysIleMetCtnrHisLeuMetGlnTyrPheProGlyAlaAsp 284
QY      661  GAGCCATTACGATGATCCTTGTCAG 684
Db      285  ValSerLeuGlnTyrProCysGln 292

RESULT 10
US-10-732-923-13628
; Sequence 13628, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15 (52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13628
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-732-923-13628

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Alignment Scores:	
Pred. No.:	3.63e-124
Score:	1215.00
Percent Similarity:	98.25%
Best Local Similarity:	96.93%
Query Match:	97.04%
DB:	17
US-09-830-144-1_COPY.408.1091 (1-684)	x US-10-732-923-13628 (1-615)
Length:	615
Matches:	221
Conservative:	3
Mismatches:	4
Indels:	0
Gaps:	0

QY	1	GTAAAGAGCTTGGGCAAGTATCCCGGTGGAAACAAATCCAAATATGTAAAGCTTATGGAGCC	60
Db	65	ValGluLeuValGluLeuSerArgValAlaHisProAsnIleValIuysLeuTyGValAla	84
QY	61	TGCTGAATCCAGATGTGTCTTGGATGGAATATGTCAGAGGGGCTCTTATATATTAATGTC	120
Db	85	CybleuAsnProValCybleuValMetGluTyAlaGluGluTyGluSerLeuTyGAsnVal	104
QY	121	CTGCATGTGCTGGAAACCAATGGCCATATTAATCTGCTGGCCCAAGCAATGAATTGGTGTGTTA	180
Db	105	LeuHisGlyAlaGluProLeuProTyTyThrAlaAlaHisIleMetSerTrpCybleu	124
QY	181	CAGTGTCCCAAGAGATGGCTTATCTTCCACAGATGCAACCCAAAGGCGCTAATTCACAG	240
Db	125	GlnCysAlaGlnGluValAlaTyTrpLeuIleSerMetCysProValAlaLeuIleHisArg	144
QY	241	GACCTGAAACCAACCAACTTACTGCTGTGGTTCAGGGGGGACAGTCTTAAAAATTTGTGAT	300
Db	145	AspLeuIuysProProAsnIleuLeuValAlaGluTyThrValIleuTyIleCysAsp	164
QY	301	TTTGTGTAACGCCGTGACATTTCAGACACACATACCAATTAACAAAGGGAGATGGCTGTGG	360
Db	165	PheGlyThrAlaCysAspIleGluIlnHisMetThrAsnIuysGluIleSerAlaAlaTrp	184
QY	361	ATGGCACTGAAGTTTGTGAAGGTAGTAATTAAGTAAAAATGTGACGCTTCACTGG	420
Db	185	MetAlaProGluValPheGluGluSerAsnTySerGluIuysCysAspValPheSerTrp	204
QY	421	GGATATATCTTTGGGAAGTAAAGACCGCGGAAACCTTTGATATAGATTTGGTGGCCCA	480
Db	205	GlyTleIleLeuTrpGluValIleThrArgArgGlySerPheAspGluIleGlyPro	224

OY	541	CCTAAGCCCATTTGAGAGCCCTGATGACCTGTTGGTCTTAAGATCCTTCCAGCGCCCT	600
Db	225	AlsbphenrgrllemettrpalaValahlsbnslrlymrhrgproProllellelyashleu	244
OY	481	GCITTCGAATCATGAGGGCTGTTTCATATAGTATGACATGCACACATGATATAAAATTTA	540
Db	225	AlsbphenrgrllemettrpalaValahlsbnslrlymrhrgproProllellelyashleu	244
OY	601	TCATATGAGGAATTTGTGAAATATATATGACTCATGATGCGGTACTTCCAGAGCAGAT	660
Db	265	SetmefclnclnulleValylsrlllemetthrshleuLysglntryrPhepfoglyAlasp	284
OY	661	GAGCCATTACAGTATCTTGTCAAG	684
Db	285	ValserleuclnlyrProcyosgln	292

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RESULT 11
US-10-732-923-13508.
; Sequence 13508, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OR INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13508
; LENGTH: 268
; TYPE: prt
; ORGANISM: Anopheles gambiae str. PBST
US-10-732-923-13508

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Alignment Scores:	
pred. No.:	2,8e-80
Score:	815.00
Percent Similarity:	77.68%
Best Local Similarity:	67.41%
Query Match:	65.10%
DB:	17
Length:	268
Matches:	151
Conservative:	23
Mismatches:	46
Indels:	4
Gaps:	3

[illegible]

QY 418 TGGGATATTCTTTGGAGATGAACGCGTGGAAACCTTTGATGAGATTGTGGC 477  
 DB 175 TTPGlyIleIleLeuTrpGluValIleAlaArgGluInProPheIleHsiIle---Asp 193  
 QY 478 CCAGCTTCCGAAATGATGGCGCTGTGCTATATGTACTCCACCCCTGATATAAAT 537  
 DB 134 ThrseryAlaIleMetIleTrpArgValHisGlnGlySerArgProIleuIleAspHis 213  
 QY 538 TTACTTAAGCCCATTTGAGAGCCTGATGACTGCTGTGTGCTTAAGATCTTCCAGAGGC 597  
 DB 214 CysProIysProIleGluGlnLeuMetValArgCysTrpAspIysAspProIleSerArg 233  
 QY 598 CCTTAATGAGGAATATGTGAAAAATATGACTACTGATGCGGACTTTCCAGAGCA 657  
 DB 234 ProSerMetIysGluValAlaSerValMetAsnAlaLeuCysIysLeuPheThrGlyGlu 253  
 QY 658 GATGAGCCATTa 669  
 DB 254 AsnGluProIle 257

## RESULT 12

US-10-664-421-136  
 ; Sequence 136, Application US/10664421  
 ; Publication No. US20040142864A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BREMER, RYAN  
 ; APPLICANT: IBRAHIM, PRABHA  
 ; APPLICANT: KUMAR, ASHITAN  
 ; APPLICANT: MANDIRAN, VALSAN  
 ; APPLICANT: MILBURN, MICHAEL V.  
 ; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE  
 ; FILE REFERENCE: 039363/0703  
 ; CURRENT APPLICATION NUMBER: US/10/664,421  
 ; PRIOR FILING DATE: 2003-09-16  
 ; APPLICANT: MILLER, JAMES  
 ; PRIOR FILING DATE: 2002-09-20  
 ; PRIOR APPLICATION NUMBER: 60/412,341  
 ; PRIOR FILING DATE: 2002-09-16  
 ; PRIOR APPLICATION NUMBER: 60/411,398  
 ; NUMBER OF SEQ ID NOS: 169  
 ; SOFTWARE: PatentIn Ver. 3.2  
 ; SEQ ID NO 136  
 ; LENGTH: 330  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-664-421-136

## Alignment Scores:

Pred. No.: 7.96e-34 Length: 330  
 Score: 392.50 Matches: 88  
 Percent Similarity: 56.68% Conservative: 35  
 Best Local Similarity: 40.55% Mismatches: 77  
 Query Match: 31.35% Indels: 17  
 DB: 16 Gaps: 6

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-10-664-421-136 (1-330)

QY 4 GAGCTTGGGAGATTATCCCTGTGAACCATCTAATATTGTAAGCTTATGAGCGCTGC 63  
 DB 66 GUAAlaArgLeuPheGlyAlaLeuGlnHisProAsnIleIleAlaLeuArgGlyAlaCys 85  
 QY 64 TTGAATCCA-----GTGTGCTTTGATGAGAAATATGCTGAAAGGGGCTCTTATATAT 117  
 DB 86 LeuAsnProIleHisLeuMetGlyValAlaArgGlyGlyAlaLeuSerArg 105  
 QY 118 GTGCTGATGCTGCTGAGAACCATTTATATCTGCTGCCAGGCAATGAGTGTCT 177  
 DB 106 ValLeuAlaGlyAlaArgValAlaProIleHisVal-----LeuValAsnTrpAla 121  
 QY 178 TTACAGGTGTTCCCAAGAGTGGCTTATCTTCAAGCATCAACCAAGCGCTAATTCAC 237  
 DB 122 ValGlnValAlaArgGlyMetAsnTrpLeuHisAsnAspAlaProValProIleIleHis 141

QY 238 AGGACCTGAACACCAACTTACTGTGTT-----GCAGCG 276  
 DB 142 ArgAspLeuSerIleAsnIleIleGlnAlaIleGluAsnHisAsnLeuAla 161  
 QY 277 GGAACGTTCTAAAAATTTGTGATTTTGTGACAGCTGTGAC---ATTGACACACATG 333  
 DB 162 AspThrValLeuLysIleThrAspPheGlyLeuAlaArgGluTrpHisLysThrLys 181  
 QY 334 ACCAATAACAAGGGAGTGTCTGTGATGAGCACTGAAGTTTGAAGTGATTAATAC 393  
 DB 182 MetSerAlaIleAlaIleThrTrpAlaTrpMetAlaProGluValIleArgLeuSerLeuPhe 201  
 QY 394 AGTAAAAATGTGACCTCTTTCAGCTGGGATATATCTTTGGAAATGAAGCGTGG 453  
 DB 202 SerLysSerSerAspValTrpSerPheGlyValLeuLeuTrpGluLeuThrGlyGlu 221  
 QY 454 AAACCTTTGATGAGATGTGTGCGCCAGCTTTCCGAATCATGTGGCTGT---CATAT 510  
 DB 222 ValProLysArgGluIle-----AspAlaLeuAlaValAlaIleTrpGlyValAlaMetAsn 239  
 QY 511 GGATCTGACACCACTGATATAAAATTTACTAGCCCATGAGACCTGATGACTGCT 570  
 DB 240 LysLeuThrLeuProIleProSerThrCysProGluProPheAlaArgLeuLeuGlu 259  
 QY 571 TGTGCTTAAAGATCTTCCAGCGCCCTTCATGAGGAATTTGAAA 621  
 DB 260 CysTrpAspProAspProIleGlyArgProAspPheGlySerIleLeuLys 276

## RESULT 13

US-10-369-022-56  
 ; Sequence 56, Application US/10369022  
 ; Publication No. US20030203847A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Millennium Pharmaceuticals, Inc.  
 ; APPLICANT: Rosenfeld, Julie Beth  
 ; APPLICANT: Silos-Santiago, Immaculada  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING  
 ; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,  
 ; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,  
 ; TITLE OF INVENTION: 27410, 33260, 4169, 15985, 69112, 2158, 224, 615, 44373,  
 ; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR  
 ; FILE REFERENCE: MP02-027P1RMONIM  
 ; CURRENT APPLICATION NUMBER: US/10/369,022  
 ; PRIOR FILING DATE: 2003-02-19  
 ; PRIOR APPLICATION NUMBER: US 60/360,495  
 ; PRIOR FILING DATE: 2002-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/370,121  
 ; PRIOR FILING DATE: 2002-04-04  
 ; PRIOR APPLICATION NUMBER: US 60/373,010  
 ; PRIOR FILING DATE: 2002-04-16  
 ; PRIOR APPLICATION NUMBER: US 60/373,908  
 ; PRIOR FILING DATE: 2002-04-19  
 ; PRIOR APPLICATION NUMBER: US 60/377,717  
 ; PRIOR FILING DATE: 2002-05-03  
 ; PRIOR APPLICATION NUMBER: US 60/379,949  
 ; PRIOR FILING DATE: 2002-05-13  
 ; PRIOR APPLICATION NUMBER: US 60/382,409  
 ; PRIOR FILING DATE: 2002-05-21  
 ; PRIOR APPLICATION NUMBER: US 60/385,280  
 ; PRIOR FILING DATE: 2002-06-03  
 ; PRIOR APPLICATION NUMBER: US 60/386,879  
 ; PRIOR FILING DATE: 2002-06-06  
 ; PRIOR APPLICATION NUMBER: US 60/387,536  
 ; PRIOR FILING DATE: 2002-06-10  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 56  
 ; LENGTH: 953  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-369-022-56

## Alignment Scores:

Pred. No.: 1.05e-33 Length: 953  
 Score: 392.50 Matches: 88  
 Percent Similarity: 56.68% Conservative: 35  
 Best Local Similarity: 40.55% Mismatches: 77  
 Query Match: 31.35% Indels: 17  
 DB: 15 Gaps: 6

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-10-369-022-56 (1-953)

```

QY 4 GACCTTGGCAGATTATCCCGTGAACCTTATATTTGTAAGCTTTATGAGCCCTGC 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 145 GlnAlaArgLeuPheGlyAlaLeuGlnHisProAsnIleIleAlaLeuAGGlyAlaCys 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 64 TTGAATCCA-----GTGTGCTTGTGATGAGATATGCTGAAGGGGCTTTATATAT 117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 165 LeuAsnProPheHisLeuGlySerLeuValMetGluTyrAlaArgGlyAlaLeuSerArg 184
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 118 GTGCTGATGCTGCTGAACCATTCCTATTTATCTGCTGCCACGCAATGAGTTGGTGT 177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 185 ValLeuAlaGlyArgValProProHisVal-----LeuValAsnTyrAla 200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 178 TTACAGTGTCCCAAGAGGTGGCTTATCTTCAAGATGCAACCCAAAGGCTATTCAC 237
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 201 ValGlnValAlaArgGlyMetAsnTyrLeuHisAsnAspAlaProValProIleIleHis 220
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 238 AGGACCTGGAACCAACCACTTACTGCTGGT-----GCAGGG 276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 221 ArgAspLeuLysSerIleAsnIleLeuIleLeuGlnAlaIleGlnAsnHisAsnLeuAla 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 277 GGAACAGTTCTAAAAATTTGTGATTTTGTACAGCTGTGAC--ATTGACACACATG 333
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 AspThrValLeuLysIleThrAspPheGlyLeuAlaArgGluTyrPheIleThrLys 260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 334 ACCAAATAACAAGGAGGATGCTGCTTGTGATGCACTGAAGTTTGAAGTATGATTAAC 393
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 261 MetSerIleAlaGlyThrTyrAlaTyrMetAlaProGluValIleArgLeuSerLeuPhe 280
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 394 AGTGAATAATGTGAGCTCTTCAGCTGGGGTATTTATCTTTGGAGATGATACCGCTCGG 453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 281 SerLysSerSerArgValIleTyrPheGlyValLeuLeuIleTyrGluLeuThrGlyGlu 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 454 AAACCTTTGATGATGATTTGTGGCCAGCTTTCCGAAATCATGTGGGCTGT--CATPAT 510
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 301 ValProTyrArgGluIle-----AspAlaLeuAlaValAlaTyrGlyValAlaMetAsn 318
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 511 GGTACTGACCAACACATGATATAAAATTTACTTAAGCCCATTTGAGAGCTGATACCTGT 570
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 319 LysLeuThrLeuProIleProSerThrCysProGluProPheAlaArgLeuGlnGlu 338
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 571 TGTGTGCTTAAAGATCTTCCAGCGCCCTTCAATGAGAGAAATTTGTGAAA 621
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 339 CysTyrAspProAspProHisGlyArgProAspPheGlySerIleLeuLys 355
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
```

## RESULT 14

US-10-042-865-98  
 Sequence 98, Application US/10042865  
 Publication No. US20040029216A1

## GENERAL INFORMATION:

GENERAL INFORMATION:  
 APPLICANT: Padigaru, Muralidhara  
 APPLICANT: Li, Li  
 APPLICANT: Zeehuseen, Bryan D  
 APPLICANT: Casman, Stacie J  
 APPLICANT: Shenoy, Suresh G  
 APPLICANT: Spytek, Kimberly  
 APPLICANT: Zhong, Mei  
 APPLICANT: Gangolli, Esna A  
 APPLICANT: Burgess, Catherine B  
 APPLICANT: Paturajan, Meera  
 APPLICANT: Verner, Corine A.M  
 APPLICANT: Taylor, Sarah  
 APPLICANT: Tchiernev, Velizar T

```

APPLICANT: Miller, Charles E
APPLICANT: Guo, Xiaojia
APPLICANT: Boldog, Ference L
APPLICANT: Grose, William M
APPLICANT: Alsobrook II, John P
APPLICANT: Gerlach, Valerie L
APPLICANT: Edinger, Shlomit R
APPLICANT: Rothenberg, Mark E
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Malyankar, Uriel M
APPLICANT: Miller, Isabelle
APPLICANT: Peyman, John
APPLICANT: Smithson, Glenda
APPLICANT: Gunther, Erik
APPLICANT: Stone, David
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
FILE REFERENCE: 21402-537
CURRENT APPLICATION NUMBER: US/10/042,865
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/260,831
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: 60/272,338
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/284,704
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 98
LENGTH: 953
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-865-98
  
```

## Alignment Scores:

Pred. No.: 1.05e-33 Length: 953  
 Score: 392.50 Matches: 88  
 Percent Similarity: 56.68% Conservative: 35  
 Best Local Similarity: 40.55% Mismatches: 77  
 Query Match: 31.35% Indels: 17  
 DB: 15 Gaps: 6

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-10-042-865-98 (1-953)

```

QY 4 GACCTTGGCAGATTATCCCGTGAACCTTATATTTGTAAGCTTTATGAGCCCTGC 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 145 GlnAlaArgLeuPheGlyAlaLeuGlnHisProAsnIleIleAlaLeuAGGlyAlaCys 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 64 TTGAATCCA-----GTGTGCTTGTGATGAGATATGCTGAAGGGGCTTTATATAT 117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 165 LeuAsnProPheHisLeuGlySerLeuValMetGluTyrAlaArgGlyAlaLeuSerArg 184
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 118 GTGCTGATGCTGCTGAACCATTCCTATTTATCTGCTGCCACGCAATGAGTTGGTGT 177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 185 ValLeuAlaGlyArgValProProHisVal-----LeuValAsnTyrAla 200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 178 TTACAGTGTCCCAAGAGGTGGCTTATCTTCAAGATGCAACCCAAAGGCTATTCAC 237
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 201 ValGlnValAlaArgGlyMetAsnTyrLeuHisAsnAspAlaProValProIleIleHis 220
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 238 AGGACCTGGAACCAACCACTTACTGCTGGT-----GCAGGG 276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 221 ArgAspLeuLysSerIleAsnIleLeuIleLeuGlnAlaIleGlnAsnHisAsnLeuAla 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 277 GGAACAGTTCTAAAAATTTGTGATTTTGTACAGCTGTGAC--ATTGACACACATG 333
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 AspThrValLeuLysIleThrAspPheGlyLeuAlaArgGluTyrPheIleThrLys 260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
```

```

QY 334 ACCAATACAGGAGGAGCTGCTGATGATGCACTGAAGTTTGAAGTAGTAATAC 393
DB 261 MetSerAlaIaGlyThrTyraIatrpMetAlaProGluValIlaArgLeuSerIeuphe 280
QY 394 AGTGAATAATGTGACGCTTTCAGCTGGGATATATTTCTTTGGAGAGTATACGGCTCG 453
DB 281 SerIysSerSerAspValItrpSerPheGlyValIleuLeuTrpGluLeuThrGlyGlu 300
QY 454 AAACCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 510
DB 301 ValProIyArgGluIle-----AspAlaLeuAlaValAlaTyrcIyValAlaMetcAsn 318
QY 511 GGTACTGCACCACTGATATTAATAATTACTAAGCCCTTGAAGCCTGATGACTCTGT 570
DB 319 LysIleuThrLeuProIleProSerThrCysProGluProPheAlaArgLeuGluGlu 338
QY 571 TGTGGTCTAAAGATCTTCCAGCGCCCTTCAATGAGAGAAATGTGAAA 621
DB 339 CysTrpAspProAspProHisGlyArgProAspPheGlySerIleLeuLys 355

RESULT 15
US-10-042-865-97
; Sequence 97, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zernhusen, Bryan D
; APPLICANT: Caeman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esba A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Verneet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tcherenev, Vellizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Grose, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: Macdougall, John
; APPLICANT: Malyankar, Ortel M
; APPLICANT: Miller, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; TIME OF INVENTION: Using the Same
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 954

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; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-042-865-97

Alignment Scores:
Pred. No.: 1,05e-33
Score: 392.50
Percent Similarity: 56.68%
Best Local Similarity: 40.55%
Query Match: 31.35%
DB: 15
Gaps: 6

US-09-830-144-1_COPY_408_1091 (1-684) x US-10-042-865-97 (1-954)

QY 4 GAGCTTGGCAGATATCCCGTGAACCTCTTAATATTGTAAGCTTATGAGCCTTGC 63
DB 145 GUAAlaArgLeuPheGlyAlaLeuGlnHisProAsnIleIleAlaLeuArgGlyAlaCys 164
QY 64 TTGAATCCA-----GTGTCTGTGATGATGATGATGATGATGATGATGATGATGAT 117
DB 165 LeuAsnProProHisIleuLysLeuValMetGluTyrAlaArgGlyAlaLeuSerArg 184
QY 118 GTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 177
DB 185 ValLeuAlaGlyArgArgValProProHisVal-----LeuValAsnTrpAla 200
QY 178 TTACAGTGTCCCAAGAGAGTGGCTTATGTCACAGCATGCAACCCAAAGCCTTAATTCAC 237
DB 201 ValGlnValAlaArgGlyMetcAsnTyrIleuHisAsnAspAlaProValProIleHis 220
QY 238 AGGAGCTGAAACCAACCAACTTACTGCTGCTT-----GCAAGG 276
DB 221 ArgAspLeuLysSerIleAsnIleLeuIleuGlnAlaIleGlnAsnHisAsnLeuAla 240
QY 277 GGGACAGTCTTAAATTTGATTTGTACAGCTGTGAC---ATTGACACACATG 333
DB 241 AspItrValLeuLysIleThrAspPheGlyLeuAlaArgGluTyrHisIlySerThrThyls 260
QY 334 ACCAATMACAGGAGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 393
DB 261 MetSerAlaIaGlyThrTyraIatrpMetAlaProGluValIlaArgLeuSerIeuphe 280
QY 394 AGTGAATAATGTGACGCTTTCAGCTGGGATATATTTCTTTGGAGAGTATACGGCTCG 453
DB 281 SerIysSerSerAspValItrpSerPheGlyValIleuLeuTrpGluLeuThrGlyGlu 300
QY 454 AAACCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 510
DB 301 ValProIyArgGluIle-----AspAlaLeuAlaValAlaTyrcIyValAlaMetcAsn 318
QY 511 GGTACTGCACCACTGATATTAATAATTACTAAGCCCTTGAAGCCTGATGACTCTGT 570
DB 319 LysIleuThrLeuProIleProSerThrCysProGluProPheAlaArgLeuGluGlu 338
QY 571 TGTGGTCTAAAGATCTTCCAGCGCCCTTCAATGAGAGAAATGTGAAA 621
DB 339 CysTrpAspProAspProHisGlyArgProAspPheGlySerIleLeuLys 355

Search completed: August 2, 2005, 20:33:28
Job time : 90.7297 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM protein - protein search, using sw model1

Run on: August 2, 2005, 20:15:38 ; Search time 27.7297 Seconds  
(without alignments)  
613.781 Million cell updates/sec

Title: US-09-830-144-2\_COPY\_76\_303

Sequence: 1 VELRQLSRVNHVNIYKLYGA.....MTILMRYFPQADEPLQYPCQ 228

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfilest.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1252	100.0	579	4	US-09-529-279-4
2	1252	100.0	579	4	US-10-158-895-4
3	1252	100.0	590	4	US-09-529-279-15
4	1252	100.0	590	4	US-10-158-895-15
5	1252	100.0	633	4	US-09-949-016-9902
6	392.5	31.3	663	4	US-09-949-016-7198
7	371	29.6	455	3	US-09-221-223-5
8	371	29.6	455	3	US-09-221-223-5
9	371	29.6	455	3	US-09-221-527-5
10	371	29.6	455	3	US-09-221-527-5
11	371	29.6	455	3	US-09-221-236-5
12	371	29.6	455	3	US-09-221-245-5
13	371	29.6	455	3	US-09-163-115-5
14	371	29.6	455	3	US-09-221-528-5
15	371	29.6	455	3	US-09-593-553-5
16	371	29.6	455	3	US-09-221-237-5
17	371	29.6	455	4	US-09-399-588-2
18	371	29.6	455	4	US-09-757-982-5
19	363.5	29.0	1036	4	US-09-345-473E-19
20	355	28.4	1036	4	US-10-014-883-2
21	355	28.4	1036	4	US-10-419-279-2
22	353.5	28.2	668	1	US-08-205-018-2
23	353.5	28.2	859	1	US-08-395-580-2
24	353.5	28.2	859	5	PCT-US95-02792-2
25	353.5	28.2	891	4	US-09-949-016-7798
26	352.5	28.2	169	4	US-09-270-767-31735
27	346	27.6	328	4	US-09-345-473E-18

28	345.5	27.6	847	4	US-09-949-016-6222	Sequence 6222, Ap
29	345.5	27.6	885	3	US-09-949-016-7789	Sequence 7789, Ap
30	338.5	27.0	835	3	US-09-291-839-2	Sequence 2, Appl
31	338.5	27.0	835	4	US-09-458-457-2	Sequence 2, Appl
32	338.5	27.0	835	4	US-09-947-199A-2	Sequence 8, Appl
33	335.5	26.8	835	4	US-09-458-457-8	Sequence 8, Appl
34	335.5	26.8	835	4	US-09-947-199A-8	Sequence 8, Appl
35	331.5	26.5	978	4	US-09-949-016-7281	Sequence 7281, Ap
36	323	25.8	821	1	US-07-928-464-2	Sequence 2, Appl
37	323	25.8	821	1	US-08-003-111B-2	Sequence 2, Appl
38	323	25.8	821	1	US-08-261-432-2	Sequence 2, Appl
39	323	25.8	821	5	PCT-US93-07347-2	Sequence 2, Appl
40	320	25.6	263	3	US-09-035-706-5	Sequence 5, Appl
41	320	25.6	263	3	US-08-955-841-5	Sequence 5, Appl
42	320	25.6	263	3	US-09-390-425-5	Sequence 5, Appl
43	320	25.6	263	3	US-09-566-906-5	Sequence 5, Appl
44	320	25.6	263	4	US-09-589-034-5	Sequence 5, Appl
45	313.5	25.0	850	4	US-09-904-389-2	Sequence 2, Appl

## ALIGNMENTS

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RESULT 1
US-09-529-279-4
; Sequence 4, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIO
; APPLICANT: TSUCHIYA, MAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529, 279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 4
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-279-4
Query Match 100.0%; Score 1252; DB 4; Length 579;
Best Local Similarity 100.0%; Pred. No. 5.2e-133;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VELRQLSRVNHVNIYKLYGACINPCLVMEYAEAGSLYVLAHGAEPLPYTAAHMSWCL 60
DB 76 VELRQLSRVNHVNIYKLYGACINPCLVMEYAEAGSLYVLAHGAEPLPYTAAHMSWCL 135
QY 61 QCSGVATLHSMOKALIHRLKPNLLVAGVTYKICDGGTACDIDHTMTNKGSAW 120
DB 136 QCSGVATLHSMOKALIHRLKPNLLVAGVTYKICDGGTACDIDHTMTNKGSAW 195
QY 121 MAPFVBSGNSYSEKCDVFSWGLIIMEVITRRKPPDEIGCAPRIMAVHNGTRPPLINL 180
DB 196 MAPFVBSGNSYSEKCDVFSWGLIIMEVITRRKPPDEIGCAPRIMAVHNGTRPPLINL 255
QY 181 KPPIBSLMTRCWSKDPSPSMETIVKIMTILMRYFPQADEPLQYPCQ 228
DB 256 KPPIBSLMTRCWSKDPSPSMETIVKIMTILMRYFPQADEPLQYPCQ 303
RESULT 2
US-10-158-895-4
; Sequence 4, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:

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/ APPLICANT: ONO, KOICHIRO
/ APPLICANT: OHTOMO, TOSHIIKO
/ APPLICANT: TSUCHIYA, MASAYUKI
/ TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
/ FILE REFERENCE: 053466/0278
/ CURRENT APPLICATION NUMBER: US/10/158,895
/ PRIOR FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: US/09/529,279
/ PRIOR FILING DATE: 2000-04-11
/ PRIOR APPLICATION NUMBER: PCT/JP98/04796
/ PRIOR FILING DATE: 1998-10-22
/ PRIOR APPLICATION NUMBER: JP 9/250188
/ PRIOR FILING DATE: 1997-10-22
/ NUMBER OF SEQ ID NOS: 48
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 579
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-158-895-4

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Query Match	100.0%	Score 1252;	DB 4;	Length 579;
Best Local Similarity	100.0%;	Pred. No. 5.2e-133;		
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QY 1 VELRLDLSRNHNIYKLVGACLNPCIVMEVYAEGLSYNVHLGAPLPYTTAAHMSCL 60

Db 76 VELRLDLSRNHNIYKLVGACLNPCIVMEVYAEGLSYNVHLGAPLPYTTAAHMSCL 135

QY 61 QCSQGVAYIHSQPKALIHRLDKPNLLVAGGYLAKICDFTGACDIOTHTMNNKSGAM 120

Db 136 QCSQGVAYIHSQPKALIHRLDKPNLLVAGGYLAKICDFTGACDIOTHTMNNKSGAM 195

QY 121 MAPEVFBSNSTSEKCDVFSWGIIMLEVITRRKPFDEIGGPAFRIWMAVHNGTRPPLIKNL 180

Db 196 MAPEVFBSNSTSEKCDVFSWGIIMLEVITRRKPFDEIGGPAFRIWMAVHNGTRPPLIKNL 255

QY 181 PKPIESLMTRCMSKDXPSORPSMEETVKIMTILMYFFPADDEPLQYPCQ 228

Db 256 PKPIESLMTRCMSKDXPSORPSMEETVKIMTILMYFFPADDEPLQYPCQ 303

RESULT 3  
US-09-529-279-15  
; Sequence 15, Application US/09529279  
Date: 09/11/2009

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? APPLICANT: ONO, KOICHIRO
? APPLICANT: OHTOMO, TOSHIHIKO
? APPLICANT: TSUCHIYA, MASAYUKI
? TITLE OF INVENTION: METHOD OF SCREENING TGF- $\beta$  INHIBITORY SUBSTANCES
? FILE REFERENCE: 053466/0278
? CURRENT APPLICATION NUMBER: US/09/529, 279
? PRIOR FILING DATE: 2000-04-11
? PRIOR APPLICATION NUMBER: PCT/JP98/04796
? PRIOR FILING DATE: 1998-10-22
? PRIOR APPLICATION NUMBER: JP 9/2290188
? PRIOR FILING DATE: 1997-10-22
? NUMBER OF SEQ ID NOS: 48
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 15
? LENGTH: 590
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-529-279-15

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Query Match	100.0%	Score 1252;	DB 4,	Length 590;																																													
Best Local Similarity	100.0%	Pred. No.5,3e-133;																																															
Matches 228;	Conservative	0;	Mismatches 0;	Indels 0;																																													
			Gaps 0;																																														
QY	1	V	E	L	D	P	L	S	R	N	H	N	I	K	L	G	A	C	N	P	C	M	E	A	B	E	G	S	L	I	N	T	L	G	A	E	P	P	T	T	A	A	A	M	S	W	L		60
Db	76	V	E	L	D	P	L	S	R	N	H	N	I	K	L	G	A	C	N	P	C	M	E	A	B	E	G	S	L	I	N	T	L	G	A	E	P	P	T	T	A	A	A	M	S	W	L		135

QY 61 QCSGVAYLHSMQPKALIHRLDKPNPLLHAGGYTLKICDFGTACDIQTHTMNNKGSAAW 120

Db 136 QCSGVAYLHSMQPKALIHRLDKPNPLLHAGGYTLKICDFGTACDIQTHTMNNKGSAAW 195

QY 121 MABVEFGSNYSSEKCVFSMGJILMEVITRRKRPDEIGGPAFRIMAAVHNGTRPPLIKUL 180

Db 196 MABVEFGSNYSSEKCDVFSWGJILMEVITRRKRPDESIGGPAFRIMAAVHNGTRPPLIKUL 255

QY 181 PKIESIMTRCWSKDSQRPSMEELVKTMTIMARVYFGADPELQYPCQ 228

Db 256 PKIESIMTRCWSKDSQRPSMEELVKTMTIMARVYFGADPELQYPCQ 303

RESULT 4  
US-10-158-895-15  
; Sequence 15, Application US/10158895  
; Patent No. CE1040

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/ APPLICANT: ONO, KOICHIRO
/ APPLICANT: OHTOMO, TOSHITAKO
/ APPLICANT: TSUCHIYA, MASAYUKI
/ TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
/ FILE REFERENCE: 053466/0278
/ CURRENT APPLICATION NUMBER: US/10/158,895
/ PRIORITY FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: US/09/529,279
/ PRIOR FILING DATE: 2000-04-11
/ PRIOR APPLICATION NUMBER: PCT/JP98/04796
/ PRIOR FILING DATE: 1998-10-22
/ PRIOR APPLICATION NUMBER: JP 9/290188
/ PRIOR FILING DATE: 1997-10-22
/ NUMBER OF SEQ. ID NOS: 48
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ. ID NO. 15
/ LENGTH: 590
/ TYPE: PR1
/ ORGANISM: Homo sapiens
/ US-10-158-895-15

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Query Match	100.0%	Score 1252;	DB 4;	Length 590;
Best Local Similarity	100.0%;	Pred. No. 5.3e-133;		
Matches 228; Conservative	0;	Mismatches 0;	Indels 0	

QY	1	VELRLQSSVNNPNIYKLYGACINLPCLMEYAEAGSLYNVLHGAEPLYYTAAAHMSCTL	60
Db	76	VELRLQSSVNNPNIYKLYGACINLPCLMEYAEAGSLYNVLHGAEPLYYTAAAHMSCTL	135
QY	61	QCSQGVATLHSMOPKALIHRLDKPPNLLVAGTVLKI CDFTACDIQTHMTNNKGSAAW	120
Db	136	QCSQGVATLHSMOPKALIHRLDKPPNLLVAGTVLKI CDFTACDIQTHMTNNKGSAAW	195
QY	121	MAPYFESNSNSEKCDVFSWGIIMBEYITRRKPPDEIGGPAFRIMAAVHNGTRPPLIKNL	180
Db	196	MAPYFESNSNSEKCDVFSWGIIMBEYITRRKPPDEIGGPAFRIMAAVHNGTRPPLIKNL	255
QY	181	PKPIESLMTRCMSKDPQSPRSMETIVKIMTHLMYFFGAABEPLOYPCQ	228
Db	256	PKPIESLMTRCMSKDPQSPRSMETIVKIMTHLMYFFGAABEPLOYPCQ	303

RESULT 5  
US-09-949-016-9902  
; Sequence 9902, Application US/09949016

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755

;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FASTSEQ for Windows Version 4.0  
;; SEQ ID NO 9902  
;; LENGTH: 633  
;; TYPE: PRF  
;; ORGANISM: Human  
US-09-949-016-9902

Query Match 100.0%; Score 1252; DB 4; Length 633;  
Best Local Similarity 100.0%; Pred. No. 5,9e-133;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VELRQLSRVNHNPVIVLYGACLNPPVCLVMEYAEAGSLYNTVLHGAEPLIPYTTAAHAMSCL 60  
DB 130 VELRQLSRVNHNPVIVLYGACLNPPVCLVMEYAEAGSLYNTVLHGAEPLIPYTTAAHAMSCL 189  
QY 61 QCSGQVAYLHSMQPKALIHRLDKPNNLLVAGTIVLKIOPGTACDIOTHTNNKGSAAW 120  
DB 190 QCSGQVAYLHSMQPKALIHRLDKPNNLLVAGTIVLKIOPGTACDIOTHTNNKGSAAW 249  
QY 121 MAPVPEGSNSYSEKCDVPSWGIILMEVITRRKPFDEIGGPAFRIMAVHNGTRPPLIKNL 180  
DB 250 MAPVPEGSNSYSEKCDVPSWGIILMEVITRRKPFDEIGGPAFRIMAVHNGTRPPLIKNL 309  
QY 181 PKPIESLMTRCMSKDPSPRSMEEIVKIMTILMRYFPDADPLDYPQ 228  
DB 310 PKPIESLMTRCMSKDPSPRSMEEIVKIMTILMRYFPDADPLDYPQ 357

RESULT 6  
US-09-949-016-7198  
;; Sequence 7198, Application US/09949016  
;; Patent No. 6812339  
;; GENERAL INFORMATION:  
;; APPLICANT: VENTER, J. Craig et al.  
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
;; FILE REFERENCE: C0001307  
;; CURRENT APPLICATION NUMBER: US/09/949,016  
;; PRIOR FILING DATE: 2000-04-14  
;; PRIOR APPLICATION NUMBER: 60/241,755  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FASTSEQ for Windows Version 4.0  
;; SEQ ID NO 7198  
;; LENGTH: 663  
;; TYPE: PRF  
;; ORGANISM: Human  
US-09-949-016-7198

Query Match 31.3%; Score 392.5; DB 4; Length 663;  
Best Local Similarity 40.6%; Pred. No. 1.7e-35;  
Matches 88; Conservative 35; Mismatches 77; Indels 17; Gaps 6;

QY 2 ELRLQSRVNHNPVIVLYGACLNPPVCLVMEYAEAGSLYNTVLHGAEPLIPYTTAAHAMSCL 59  
DB 198 ELRLQSRVNHNPVIVLYGACLNPPVCLVMEYAEAGSLYNTVLHGAEPLIPYTTAAHAMSCL 253  
QY 60 LQCSGQVAYLHSMQPKALIHRLDKPNNLLV-----AGTIVLKIOPGTACDIOTHTNM 111  
DB 254 VQVAGMYLHNDADVPIIHRDLKSNILILILAIENHNILADIVLKITDGLAREWHKTYK 313  
QY 112 TNNKSAAMMAPEVEGNSYSEKCDVPSWGIILMEVITRRKPFDEIGGPAFRIMAV-HN 170

DB 314 MSAAGTYAMAPREVILSLFSKSDVMSFGVLLMELLTGSEVPYREI--DALAVAGVAMN 371  
QY 171 GTRPPLIKLKPPIESLMTRCMSKDPSPRSMEEIVK 207  
DB 372 KTLPIPTCTCPBPFAHLEECWDPDGRBDFGSILK 408

RESULT 7  
US-09-221-235-5  
;; Sequence 5, Application US/09221235  
;; Patent No. 6043040  
;; GENERAL INFORMATION:  
;; APPLICANT: Acton, Susan  
;; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
;; FILE REFERENCE: NMI-050  
;; CURRENT APPLICATION NUMBER: US/09/221,235  
;; CURRENT FILING DATE: 1998-12-28  
;; EARLIER APPLICATION NUMBER: 09/163,115  
;; EARLIER FILING DATE:  
;; NUMBER OF SEQ ID NOS: 15  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 5  
;; LENGTH: 455  
;; TYPE: PRF  
;; ORGANISM: Homo sapiens  
US-09-221-235-5

Query Match 29.6%; Score 371; DB 3; Length 455;  
Best Local Similarity 37.7%; Pred. No. 2.6e-33;  
Matches 81; Conservative 40; Mismatches 80; Indels 14; Gaps 8;

QY 2 ELRLQSRVNHNPVIVLYGACLNPPVCLVMEYAEAGSLYNTVLHGAEPLIPYTTAAHAMS 57  
DB 53 EARLISVLSHNNIIQFYGVILBPPNNGIVTEYASIGSLYDINSNRSEEM---DMDHMT 109  
QY 58 WCLQCSGQVAYLHSMQPKALIHRLDKPNNLLVAGTIVLKIOPGTACDIOTHTNNK-- 115  
DB 110 WATVAGKMYLHNEAPVYVYHRLDKSRNVVIAADG-VLKICDYG-ASRFNHTTHMSLV 167  
QY 116 GSAAMMAPEVEGNSYSEKCDVPSWGIILMEVITRRKPFDEIGGPAFRIMV-AVHNGTRP 174  
DB 168 GTFPMMAPEVYQSLPVBETDYSYGVAVLWMLTRVYVFGKLBG-LQVAVLVEKQERL 225  
QY 175 PLIKLKPPIESLMTRCMSKDPSPRSMEEIVKIM 209  
DB 226 TTPSCRSRPAELHQCWEADAKGRBPFKQIISIL 260

RESULT 8  
US-09-221-928-5  
;; Sequence 5, Application US/09221928  
;; Patent No. 6121030  
;; GENERAL INFORMATION:  
;; APPLICANT: Acton, Susan  
;; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
;; FILE REFERENCE: NMI-050  
;; CURRENT APPLICATION NUMBER: US/09/221,928  
;; CURRENT FILING DATE: 1998-12-28  
;; EARLIER APPLICATION NUMBER: 09/163,115  
;; EARLIER FILING DATE:  
;; NUMBER OF SEQ ID NOS: 15  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 5  
;; LENGTH: 455  
;; TYPE: PRF  
;; ORGANISM: Homo sapiens  
US-09-221-928-5

Query Match 29.6%; Score 371; DB 3; Length 455;  
Best Local Similarity 37.7%; Pred. No. 2.6e-33;  
Matches 81; Conservative 40; Mismatches 80; Indels 14; Gaps 8;

QY 2 ELRLQSRVNHNPVIVLYGACLNPPVCLVMEYAEAGSLYNTVLHGAEPLIPYTTAAHAMS 57



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Qy      58 WCLQCSQGVAVYLSHMQPKALIHRLDKPNNLLVAGGTVLKICDFGTACDIQTHMTNNK-- 115
Db      110 WATDVAKGMHYLHMEAPVYVHRLDKSRNVVIAADG-VLKICDFG-ASRFHNHTTHMSLV 167
Qy      116 GSAAMMAPEVFECSNYSEKCDVFSWGIIIMEVITRRKPPDEIGPAPRIMW-AVHNGTRP 174
Db      168 GTFPMMAPEVIOQLPVSETCDITYSGVVLMEMLTREVFPKGLG--LQVAMLVVERKNERL 225
Qy      175 PLIKNLKPRIEISLMTRCWSKDPSPQSPMEIYKIM 209
Db      226 TIPSSCPSPFAELHQCEWADAKKRPSPKQIISIL 260
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RESULT 9
US-09-221-527-5
; Sequence 5, Application US/09221527
; Patent No. 6146832
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,527
; EARLIER FILING DATE: 1998-12-28
; EARLIER FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-527-5
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Query Match      29.6%; Score 371; DB 3; Length 455;
Best Local Similarity 37.7%; Pred. No. 2.6e-33;
Matches 81; Conservative 40; Mismatches 80; Indels 14; Gaps 8;
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Qy      2 ELRLQSRVNHNIYKLYGACINP--VCLVMEYAEAGSLVNVHLG--AEPLPYTTAAHAMS 57
Db      53 EABLISVLSHRNIIQFYGVILEPNNYGIETVYASIGSLVDYINSNRSEEM--DMDHIMT 109
Qy      58 WCLQCSQGVAVYLSHMQPKALIHRLDKPNNLLVAGGTVLKICDFGTACDIQTHMTNNK-- 115
Db      110 WATDVAKGMHYLHMEAPVYVHRLDKSRNVVIAADG-VLKICDFG-ASRFHNHTTHMSLV 167
Qy      116 GSAAMMAPEVFECSNYSEKCDVFSWGIIIMEVITRRKPPDEIGPAPRIMW-AVHNGTRP 174
Db      168 GTFPMMAPEVIOQLPVSETCDITYSGVVLMEMLTREVFPKGLG--LQVAMLVVERKNERL 225
Qy      175 PLIKNLKPRIEISLMTRCWSKDPSPQSPMEIYKIM 209
Db      226 TIPSSCPSPFAELHQCEWADAKKRPSPKQIISIL 260
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RESULT 10
US-09-221-236-5
; Sequence 5, Application US/09221236
; Patent No. 6146841
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,236
; EARLIER FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-236-5
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Query Match      29.6%; Score 371; DB 3; Length 455;
Best Local Similarity 37.7%; Pred. No. 2.6e-33;
Matches 81; Conservative 40; Mismatches 80; Indels 14; Gaps 8;

Qy      2 ELRLQSRVNHNIYKLYGACINP--VCLVMEYAEAGSLVNVHLG--AEPLPYTTAAHAMS 57
Db      53 EABLISVLSHRNIIQFYGVILEPNNYGIETVYASIGSLVDYINSNRSEEM--DMDHIMT 109
Qy      58 WCLQCSQGVAVYLSHMQPKALIHRLDKPNNLLVAGGTVLKICDFGTACDIQTHMTNNK-- 115
Db      110 WATDVAKGMHYLHMEAPVYVHRLDKSRNVVIAADG-VLKICDFG-ASRFHNHTTHMSLV 167
Qy      116 GSAAMMAPEVFECSNYSEKCDVFSWGIIIMEVITRRKPPDEIGPAPRIMW-AVHNGTRP 174
Db      168 GTFPMMAPEVIOQLPVSETCDITYSGVVLMEMLTREVFPKGLG--LQVAMLVVERKNERL 225
Qy      175 PLIKNLKPRIEISLMTRCWSKDPSPQSPMEIYKIM 209
Db      226 TIPSSCPSPFAELHQCEWADAKKRPSPKQIISIL 260
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RESULT 11
US-09-221-416-5
; Sequence 5, Application US/09221416
; Patent No. 6153417
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,416
; EARLIER FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-416-5
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Query Match      29.6%; Score 371; DB 3; Length 455;
Best Local Similarity 37.7%; Pred. No. 2.6e-33;
Matches 81; Conservative 40; Mismatches 80; Indels 14; Gaps 8;
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Qy      2 ELRLQSRVNHNIYKLYGACINP--VCLVMEYAEAGSLVNVHLG--AEPLPYTTAAHAMS 57
Db      53 EABLISVLSHRNIIQFYGVILEPNNYGIETVYASIGSLVDYINSNRSEEM--DMDHIMT 109
Qy      58 WCLQCSQGVAVYLSHMQPKALIHRLDKPNNLLVAGGTVLKICDFGTACDIQTHMTNNK-- 115
Db      110 WATDVAKGMHYLHMEAPVYVHRLDKSRNVVIAADG-VLKICDFG-ASRFHNHTTHMSLV 167
Qy      116 GSAAMMAPEVFECSNYSEKCDVFSWGIIIMEVITRRKPPDEIGPAPRIMW-AVHNGTRP 174
Db      168 GTFPMMAPEVIOQLPVSETCDITYSGVVLMEMLTREVFPKGLG--LQVAMLVVERKNERL 225
Qy      175 PLIKNLKPRIEISLMTRCWSKDPSPQSPMEIYKIM 209
Db      226 TIPSSCPSPFAELHQCEWADAKKRPSPKQIISIL 260
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RESULT 12
US-09-221-245-5
; Sequence 5, Application US/09221245
; Patent No. 6180358
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
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Qy 116 GSAAMWAPVFEVSGSNYSKCDVPSWGIIMWEVITRRKPPDEIGPAPRIMW-AVANGTRP 174  
Db 168 GTFPMWAPVFIQSLPVSETCDTYSYGVLMEMLTREVPPKLEGG--LOVAMLVEKNERL 225  
Qy 175 PLIKNLPKPIESIMTRCWSKDPSPORPSMEIVKIM 209  
Db 226 TIPSOCPRGFALHQCWEADAKKRPSFKQITISIL 260

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Job time : 28.7297 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 2, 2005, 20:29:48 ; Search time 83.9595 Seconds

(without alignments)  
1058.018 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

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- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1252	100.0	336	16	US-10-664-421-135
2	1252	100.0	518	14	US-10-283-023-2
3	1252	100.0	518	15	US-10-386-414-13
4	1252	100.0	579	13	US-10-158-895-4
5	1252	100.0	579	14	US-10-384-743-4
6	1252	100.0	590	13	US-10-158-895-15
7	1252	100.0	590	14	US-10-384-743-15
8	1233.5	98.5	623	17	US-10-732-923-13442
9	1221	97.5	616	17	US-10-732-923-13629
10	1215	97.0	615	17	US-10-732-923-13628
11	815	65.1	268	17	US-10-732-923-13508

12	392.5	31.3	330	16	US-10-664-421-136	Sequence 136, App
13	392.5	31.3	953	15	US-10-369-022-56	Sequence 56, Appl
14	392.5	31.3	954	15	US-10-042-865-98	Sequence 98, Appl
15	392.5	31.3	954	15	US-10-042-865-97	Sequence 97, Appl
16	392.5	31.3	954	15	US-10-263-929-187	Sequence 187, App
17	387.5	31.0	940	18	US-10-840-512-223	Sequence 223, App
18	387.5	31.0	1018	17	US-10-732-923-13436	Sequence 13436, A
19	379	30.3	422	16	US-10-437-963-13604	Sequence 13604, A
20	377	30.1	376	16	US-10-437-963-13612	Sequence 13612, A
21	376	30.0	371	17	US-10-732-923-13608	Sequence 13608, A
22	374.5	29.9	376	15	US-10-424-599-271998	Sequence 271998, A
23	374.5	29.9	2964	17	US-10-732-923-13552	Sequence 13552, A
24	373.5	29.8	603	16	US-10-437-963-135923	Sequence 135923, A
25	373	29.8	357	15	US-10-424-599-252964	Sequence 252964, A
26	373	29.8	415	16	US-10-425-115-351552	Sequence 351552, A
27	373	29.8	426	15	US-10-425-114-60778	Sequence 60778, A
28	373	29.8	433	15	US-10-425-114-57936	Sequence 57936, A
29	372	29.7	289	17	US-10-732-923-13427	Sequence 13427, A
30	372	29.7	415	16	US-10-425-115-351548	Sequence 351548, A
31	372	29.7	426	15	US-10-425-114-55173	Sequence 55173, A
32	372	29.7	454	17	US-10-732-923-13428	Sequence 13428, A
33	372	29.7	802	17	US-10-732-923-13428	Sequence 13428, A
34	372	29.6	312	16	US-10-664-421-137	Sequence 137, App
35	371	29.6	349	14	US-10-106-698-6345	Sequence 6345, App
36	371	29.6	417	15	US-10-425-114-46822	Sequence 46822, A
37	371	29.6	455	9	US-09-757-982-5	Sequence 5, Appl
38	371	29.6	455	15	US-10-094-749-2477	Sequence 2477, Ap
39	371	29.6	455	15	US-10-352-674A-2	Sequence 2, Appl
40	371	29.6	455	17	US-10-786-501-5	Sequence 5, Appl
41	371	29.6	473	15	US-10-296-115-837	Sequence 837, App
42	371	29.6	800	16	US-10-408-765A-1101	Sequence 1101, App
43	371	29.6	800	16	US-10-737-650-66	Sequence 66, Appl
44	371	29.6	800	16	US-10-737-650-66	Sequence 66, Appl
45	371	29.6	800	16	US-10-751-736-64	Sequence 64, Appl

#### ALIGNMENTS

RESULT 1  
US-10-664-421-135 Application US/10664421  
; Sequence 135, Application No. US20040142864A1  
; Publication No. US20040142864A1  
; GENERAL INFORMATION:  
; APPLICANT: BREMER, RYAN  
; APPLICANT: IBRAHIM, PRABHA  
; APPLICANT: KUMAR, ABHINAV  
; APPLICANT: MANDIVAN, VALSAN  
; APPLICANT: MILBURN, MICHAEL V.  
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE  
; FILE REFERENCE: 039363/0703  
; CURRENT APPLICATION NUMBER: US/10/664,421  
; CURRENT FILING DATE: 2003-09-16  
; PRIOR APPLICATION NUMBER: 60/412,341  
; PRIOR FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: 60/411,398  
; PRIOR FILING DATE: 2002-09-16  
; NUMBER OF SEQ ID NOS: 169  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 135  
; LENGTH: 336  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-664-421-135

Query Match 100.0%; Score 1252; DB 16; Length 336;  
Best Local Similarity 100.0%; Pred. No. 2e-110;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VELRLQSLRVNHPNIVKLYGCAINPCVLYMEFAEGSLVNTLHGAEPLRYTAAHAMSQCL 60  
DB 76 VELRLQSLRVNHPNIVKLYGCAINPCVLYMEFAEGSLVNTLHGAEPLRYTAAHAMSQCL 135

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QY 61 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGTVCICDPFGTACDIQTHMTNNKGSAAW 120
| 136 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGTVCICDPFGTACDIQTHMTNNKGSAAW 195
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QY 121 MAPEVEGNSYSEKCDVFSWGIILMEVITRRKPFDEIGGPAFRIMAVHNGTRPPLIKNL 180
| 196 MAPEVEGNSYSEKCDVFSWGIILMEVITRRKPFDEIGGPAFRIMAVHNGTRPPLIKNL 255
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QY 181 PKPIESLMTRCWSKDPSPRSMEIYKIMTHLMRYFPGADEPLQYPCQ 228
| 256 PKPIESLMTRCWSKDPSPRSMEIYKIMTHLMRYFPGADEPLQYPCQ 303
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## RESULT 2

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US-10-283-023-2
; Sequence 2, Application US/10283023
; Publication No. US20030091573A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: Methods and compositions for the
; TITLE OF INVENTION: diagnosis and treatment of hematological disorders using
; FILE REFERENCE: MP101-239P1RM
; CURRENT APPLICATION NUMBER: US/10/283,023
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-283-023-2
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Query Match 100.0%; Score 1252; DB 14; Length 518;
Best Local Similarity 100.0%; Pred. No. 3.3e-110;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VELRLSRVNHNPNIYKLYGACLNPCVCLVMEYABGSLYNTLHGAEPPLPYTTAAHANSWCL 60
| 76 VELRLSRVNHNPNIYKLYGACLNPCVCLVMEYABGSLYNTLHGAEPPLPYTTAAHANSWCL 135
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QY 61 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGTVCICDPFGTACDIQTHMTNNKGSAAW 120
| 136 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGTVCICDPFGTACDIQTHMTNNKGSAAW 195
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QY 121 MAPEVEGNSYSEKCDVFSWGIILMEVITRRKPFDEIGGPAFRIMAVHNGTRPPLIKNL 180
| 196 MAPEVEGNSYSEKCDVFSWGIILMEVITRRKPFDEIGGPAFRIMAVHNGTRPPLIKNL 255
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QY 181 PKPIESLMTRCWSKDPSPRSMEIYKIMTHLMRYFPGADEPLQYPCQ 228
| 256 PKPIESLMTRCWSKDPSPRSMEIYKIMTHLMRYFPGADEPLQYPCQ 303
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## RESULT 3

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US-10-386-414-13
; Sequence 13, Application US/10386414
; Publication No. US20040006016A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Liebermann, Rosana
; APPLICANT: Robison, Keith E.
; APPLICANT: White, David
; APPLICANT: Williamson, Mark W.
; APPLICANT: Cook, William James
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Chun, Myoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
; TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MP103-0210MNTM
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; CURRENT APPLICATION NUMBER: US/10/386,414
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/254,037
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/833,082
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-386-414-13
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Query Match 100.0%; Score 1252; DB 15; Length 518;
Best Local Similarity 100.0%; Pred. No. 3.3e-110;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 181 PKPIESLMTRCWSKDPSPRSMEIYKIMTHLMRYFPGADEPLQYPCQ 228
| 256 PKPIESLMTRCWSKDPSPRSMEIYKIMTHLMRYFPGADEPLQYPCQ 303
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## RESULT 4

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US-10-158-895-4
; Sequence 4, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHITAKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 579
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TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-4

Query Match 100.0%; Score 1252; DB 13; Length 579;  
Best Local Similarity 100.0%; Pred. No. 3,7e-110;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 196 MAPEVFGSNYSSEKCDVFSMGIIIMEVITRRKPPDEIGGPAFRIMMAVHNGTRPPLIKNL 255  
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DB 256 PKPIESLMTRCWSKDPSPQSPSMERIIVKIMTHLMRYFPGADEPLQYPCQ 303

RESULT 5  
US-10-384-743-4  
Sequence 4, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHITAKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384, 743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529, 279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-384-743-4

Query Match 100.0%; Score 1252; DB 14; Length 579;  
Best Local Similarity 100.0%; Pred. No. 3,7e-110;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 76 VELRQLSRVNHNPNIIVKLYGACINPVCIMVEYAEAGSLYNYLHGAEPPLPYTAAHAMSACL 135  
QY 61 QCSGVAYLHSMOPKALIHDLKPPNLLVAGGTVLKICDGTACDIQTHMTNKGSAAM 120  
DB 136 QCSGVAYLHSMOPKALIHDLKPPNLLVAGGTVLKICDGTACDIQTHMTNKGSAAM 195  
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DB 196 MAPEVFGSNYSSEKCDVFSMGIIIMEVITRRKPPDEIGGPAFRIMMAVHNGTRPPLIKNL 255  
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DB 256 PKPIESLMTRCWSKDPSPQSPSMERIIVKIMTHLMRYFPGADEPLQYPCQ 303

RESULT 6

US-10-158-895-15  
Sequence 15, Application US/10158895  
Publication No. US20020155624A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHITAKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158, 895  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529, 279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 590  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-15

Query Match 100.0%; Score 1252; DB 13; Length 590;  
Best Local Similarity 100.0%; Pred. No. 3,8e-110;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VELRQLSRVNHNPNIIVKLYGACINPVCIMVEYAEAGSLYNYLHGAEPPLPYTAAHAMSACL 60  
DB 76 VELRQLSRVNHNPNIIVKLYGACINPVCIMVEYAEAGSLYNYLHGAEPPLPYTAAHAMSACL 135  
QY 61 QCSGVAYLHSMOPKALIHDLKPPNLLVAGGTVLKICDGTACDIQTHMTNKGSAAM 120  
DB 136 QCSGVAYLHSMOPKALIHDLKPPNLLVAGGTVLKICDGTACDIQTHMTNKGSAAM 195  
QY 121 MAPEVFGSNYSSEKCDVFSMGIIIMEVITRRKPPDEIGGPAFRIMMAVHNGTRPPLIKNL 180  
DB 196 MAPEVFGSNYSSEKCDVFSMGIIIMEVITRRKPPDEIGGPAFRIMMAVHNGTRPPLIKNL 255  
QY 181 PKPIESLMTRCWSKDPSPQSPSMERIIVKIMTHLMRYFPGADEPLQYPCQ 228  
DB 256 PKPIESLMTRCWSKDPSPQSPSMERIIVKIMTHLMRYFPGADEPLQYPCQ 303

RESULT 7  
US-10-384-743-15  
Sequence 15, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHITAKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384, 743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529, 279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 590  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-384-743-15

Query Match 100.0%; Score 1252; DB 14; Length 590;

Best Local Similarity 100.0%; Pred. No. 3.8e-110; Indels 0; Gaps 0;  
Matches 228; Conservative 0; Mismatches 0;

QY 1 VELRQLSRVNHPIVLYGACINPVCVLMVEYAGGSLYNYVHGAEPPLPYTTAAHMSWCL 60  
Db 76 VELRQLSRVNHPIVLYGACINPVCVLMVEYAGGSLYNYVHGAEPPLPYTTAAHMSWCL 135  
QY 61 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTACDIOHTMTNNKGSAAW 120  
Db 136 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTACDIOHTMTNNKGSAAW 195  
QY 121 MAPEVFGSNYSKCDVFSWGIIIMVEVITRRKPFDEIGGAPRIMAAVHNGTRPPLIKNL 180  
Db 196 MAPEVFGSNYSKCDVFSWGIIIMVEVITRRKPFDEIGGAPRIMAAVHNGTRPPLIKNL 255  
QY 181 PKPISLMTRCWSKDPORPSMEEIVKIMTHLMRYFGADEPLQYPCQ 228  
Db 256 PKPISLMTRCWSKDPORPSMEEIVKIMTHLMRYFGADEPLQYPCQ 303

## RESULT 8

US-10-732-923-13442  
; Sequence 13442, Application US/10732923  
; Publication No. US20050108791A1  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923  
; PRIOR FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO 13442  
; LENGTH: 623  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-732-923-13442

Query Match 98.5%; Score 123.5; DB 17; Length 623;  
Best Local Similarity 93.1%; Pred. No. 2.3e-108;  
Matches 228; Conservative 0; Mismatches 0; Indels 17; Gaps 1;

QY 1 VELRQLSRVNHPIVLYGACINPVCVLMVEYAGGSLYNYVHGAEPPLPYTTAAHMSWCL 60  
Db 76 VELRQLSRVNHPIVLYGACINPVCVLMVEYAGGSLYNYVHGAEPPLPYTTAAHMSWCL 135  
QY 61 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTACDIOHTMTNNKGSAAW 120  
Db 136 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTACDIOHTMTNNKGSAAW 195  
QY 121 MAPEVFGSNYSKCDVFSWGIIIMVEVITRRKPFDEIGGAPRIMAAVHNGTRPPLIKNL 180  
Db 196 MAPEVFGSNYSKCDVFSWGIIIMVEVITRRKPFDEIGGAPRIMAAVHNGTRPPLIKNL 255  
QY 181 PKPISLMTRCWSKDPORPSMEEIVKIMTHLMRYFGADEPLQYPCQ 223  
Db 256 PKPISLMTRCWSKDPORPSMEEIVKIMTHLMRYFGADEPLQYPCQ 315  
QY 224 QYPCQ 228  
Db 316 QYPCQ 320

## RESULT 9

US-10-732-923-13629  
; Sequence 13629, Application US/10732923  
; Publication No. US20050108791A1  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923

; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154  
; PRIOR FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO 13629  
; LENGTH: 616  
; TYPE: PRT  
; ORGANISM: Xenopus laevis  
US-10-732-923-13629

Query Match 97.5%; Score 1221; DB 17; Length 616;  
Best Local Similarity 97.4%; Pred. No. 3.5e-107;  
Matches 222; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VELRQLSRVNHPIVLYGACINPVCVLMVEYAGGSLYNYVHGAEPPLPYTTAAHMSWCL 60  
Db 65 VELRQLSRVNHPIVLYGACINPVCVLMVEYAGGSLYNYVHGAEPPLPYTTAAHMSWCL 124  
QY 61 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTACDIOHTMTNNKGSAAW 120  
Db 125 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTACDIOHTMTNNKGSAAW 184  
QY 121 MAPEVFGSNYSKCDVFSWGIIIMVEVITRRKPFDEIGGAPRIMAAVHNGTRPPLIKNL 180  
Db 185 MAPEVFGSNYSKCDVFSWGIIIMVEVITRRKPFDEIGGAPRIMAAVHNGTRPPLIKNL 244  
QY 181 PKPISLMTRCWSKDPORPSMEEIVKIMTHLMRYFGADEPLQYPCQ 228  
Db 245 PKPISLMTRCWSKDPORPSMEEIVKIMTHLMRYFGADEPLQYPCQ 292

## RESULT 10

US-10-732-923-13628  
; Sequence 13628, Application US/10732923  
; Publication No. US20050108791A1  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923  
; PRIOR FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO 13628  
; LENGTH: 615  
; TYPE: PRT  
; ORGANISM: Xenopus laevis  
US-10-732-923-13628

Query Match 97.0%; Score 1215; DB 17; Length 615;  
Best Local Similarity 96.9%; Pred. No. 1.3e-106;  
Matches 221; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 VELRQLSRVNHPIVLYGACINPVCVLMVEYAGGSLYNYVHGAEPPLPYTTAAHMSWCL 60  
Db 65 VELRQLSRVNHPIVLYGACINPVCVLMVEYAGGSLYNYVHGAEPPLPYTTAAHMSWCL 124  
QY 61 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTACDIOHTMTNNKGSAAW 120  
Db 125 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTACDIOHTMTNNKGSAAW 184  
QY 121 MAPEVFGSNYSKCDVFSWGIIIMVEVITRRKPFDEIGGAPRIMAAVHNGTRPPLIKNL 180  
Db 185 MAPEVFGSNYSKCDVFSWGIIIMVEVITRRKPFDEIGGAPRIMAAVHNGTRPPLIKNL 244  
QY 181 PKPISLMTRCWSKDPORPSMEEIVKIMTHLMRYFGADEPLQYPCQ 228  
Db 245 PKPISLMTRCWSKDPORPSMEEIVKIMTHLMRYFGADEPLQYPCQ 292

## RESULT 11

US-10-732-923-13508







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Db      145 EARLFGALQHFNITIALRGACINPPLCLVMEYARGALSRYLAGRVRPHV---LVNWA 200
QY      60 LQCSQGVAYLHSMQPKALIHRLKPNLLV-----AGGTVALKICDFTACD-IQTHM 111
Db      201 VQVARGMNYLHNDAPVPIIHRDLKSINILLIEAIEENHNLADTVLKITDFGLAREMHKTK 260
QY      112 TNNKGAAMWAPVEEGSNYSEKCDVPSWGIILWEVITRRKPDDEIGGPAFRIMWV-HN 170
Db      261 MSAAGTYAMWAPVIRLSLFSKSSDVWSFGVLLWELLGAVYRRI--DALAVAYGVAMN 318
QY      171 GTRPPLIKNLPKPIESLMTRCMSKDPQSOPSMEEIVK 207
Db      319 KLTIPISPTCPFPARLIEECWDPDPHGRPDGSIK 355

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Search completed: August 2, 2005, 20:42:13  
 Job time : 84.9595 secs

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## OM protein - nucleic search, using frame\_plus.p2n model

Run on: August 2, 2005, 20:33:39 ; Search time 229.541 Seconds

(without alignments)  
1625.295 Million cell updates/sec

Title: US-09-830-144-2\_COPY\_76\_303  
Perfect score: 1252  
Sequence: 1 VERBOLSRVHPRIVKLYGA.....MTHLMRYFGADREPLQYPCQ 228

Scoring table:  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

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-O=/cgmt2/USPFO.spool/US09830144/funat.02082005.101155.12556/app.query.fasta\_1.654  
-DB=issued Patents NA -OPMT=fastap -SUPFIX=p2n.rnt -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdd  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Issued Patents NA:  
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2: /cgmt2\_6/ptodata/1/ina/5B.COMB.seq:\*  
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5: /cgmt2\_6/ptodata/1/ina/6C.COMB.seq:\*  
6: /cgmt2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1252	100.0	1788	3	US-09-529-279-14
2	1252	100.0	1788	4	US-10-158-895-14
3	1252	100.0	2656	2	US-08-685-625A-5
4	1252	100.0	2656	3	US-09-529-279-3
5	1252	100.0	2656	4	US-10-158-895-3
6	1252	100.0	2769	4	US-09-949-016-4031
7	1247	99.6	2443	2	US-08-685-625A-1
8	392.5	31.3	3143	4	US-09-949-016-1327
9	371	29.6	1365	3	US-09-221-235-6
10	371	29.6	1365	3	US-09-221-928-6
11	371	29.6	1365	3	US-09-221-527-6
12	371	29.6	1365	3	US-09-221-236-6

13	371	29.6	1365	3	US-09-221-416-6	Sequence 6, Appli
14	371	29.6	1365	3	US-09-221-245-6	Sequence 6, Appli
15	371	29.6	1365	3	US-09-163-115-6	Sequence 6, Appli
16	371	29.6	1365	3	US-09-221-528-6	Sequence 6, Appli
17	371	29.6	1365	3	US-09-593-553-6	Sequence 6, Appli
18	371	29.6	1365	3	US-09-221-237-6	Sequence 6, Appli
19	371	29.6	1365	4	US-09-757-982-6	Sequence 6, Appli
20	371	29.6	2119	4	US-09-399-588-1	Sequence 1, Appli
21	371	29.6	2120	3	US-09-221-235-4	Sequence 4, Appli
22	371	29.6	2120	3	US-09-221-928-4	Sequence 4, Appli
23	371	29.6	2120	3	US-09-221-527-4	Sequence 4, Appli
24	371	29.6	2120	3	US-09-221-336-4	Sequence 4, Appli
25	371	29.6	2120	3	US-09-221-116-4	Sequence 4, Appli
26	371	29.6	2120	3	US-09-221-245-4	Sequence 4, Appli
27	371	29.6	2120	3	US-09-163-115-4	Sequence 4, Appli
28	371	29.6	2120	3	US-09-221-528-4	Sequence 4, Appli
29	371	29.6	2120	3	US-09-593-553-4	Sequence 4, Appli
30	371	29.6	2120	3	US-09-221-237-4	Sequence 4, Appli
31	371	29.6	2120	4	US-09-757-982-4	Sequence 4, Appli
32	355	28.4	3111	4	US-10-014-882-1	Sequence 1, Appli
33	355	28.4	3111	4	US-10-014-882-1	Sequence 1, Appli
34	355	28.4	3518	4	US-10-014-882-3	Sequence 3, Appli
35	355	28.4	3518	4	US-10-014-882-3	Sequence 3, Appli
36	353.5	28.2	3364	4	US-09-949-016-1927	Sequence 1927, Ap
37	353.5	28.2	3389	1	US-08-395-580-1	Sequence 1, Appli
38	353.5	28.2	3426	1	US-08-205-018-1	Sequence 106, App
39	352.5	28.2	507	4	US-09-270-767-106	Sequence 15389, A
40	352.5	28.2	507	4	US-09-270-767-106	Sequence 15389, A
41	345.5	27.6	3558	4	US-09-949-016-151	Sequence 1518, Ap
42	345.5	27.6	3558	4	US-09-949-016-151	Sequence 1518, Ap
43	338.5	27.0	2505	3	US-09-291-839-3	Sequence 3, Appli
44	338.5	27.0	2505	4	US-09-458-457-3	Sequence 3, Appli
45	338.5	27.0	2505	4	US-09-947-199A-3	Sequence 3, Appli

## ALIGNMENTS

RESULT 1  
US-09-529-279-14  
; Sequence 14, Application US/09529279  
; Patent No. 6451617  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHIOHKO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/09/529, 279  
; CURRENT FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: JP 9/290188  
; PRIOR FILING DATE: 1997-10-22  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 1788  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (7)..(1776)  
US-09-529-279-14  
Alignment Scores:  
Pred. No.: 9.04e-146  
Score: 1252.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Length: 1788  
Matches: 228  
Mismatch: 0  
Indels: 0  
Gaps: 0  
US-09-830-144-2\_COPY\_76\_303 (1-228) x US-09-529-279-14 (1-1788)

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QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIleLeuTyrGlyAla 20
Db 232 GTAGACCTTCGGCAGTTATCCCGTGAACCAATCTTAATATTGTAAAGCTTTATGAGCC 291
QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40
Db 292 TCGTTGAATCCAGTGTCTTGTGATGAAATATGCGAAGGGGGCTCTTTATATATATG 351
QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
Db 352 CTGCATGTGTGTAACCATTCATATATATCTGCTGCCCAAGCAATGAGTTGGTTT 411
QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProValAlaLeuIleHisArg 80
Db 412 CAGTGTTCACAGAGAGTGGCTTATCTTCACAGCAAGCAACCAAGCGCTAATTCACAG 471
QY 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuValIleCysAsp 100
Db 472 GACCTGAACCAACCAACTTACTGCTGGTGCAGGGGGGCAAGTTCTTAAATAATTTGAT 531
QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 120
Db 532 TTGGGTACAGCCTGTGAATTCACACACATGACCAATTAACAAGGGAGTGTGCTGG 591
QY 121 MetAlaProGluValPheGlyGlySerAsnTyrSerGluLysCysAspValPheSerTyr 140
Db 592 ATGGACCTGAAGTTTGAAGTATGATTAACATGTAATAATGTAAGTGTGCTGG 651
QY 141 GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyPro 160
Db 652 GGTATATATCTTGTGGAGATGATACGGTGCAGAAACCTTTGATGATGGTGGCCCA 711
QY 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProPheLeuIleValAsnLeu 180
Db 712 GCTTTCGAAATCAGTGTGGCTGTCTCATATATGATCTGCAGCACCATGATTAATAATTTA 771
QY 181 ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 200
Db 772 CCTAAGCCCATGTGAGACCTGATGACTCGTGTGGCTTAAAGATCTTCCAGGCCCT 831
QY 201 SerMetGluGluIleValIleValIleMetThrHisLeuMetLysGlyPheProGlyAlaAsp 220
Db 832 TCATATGAGAAATTTGTGAATAATATGACTCACTTATGCGTACTTTCCAGAGCAGAT 891
QY 221 GluProLeuGlnTyrProCysGln 228
Db 892 GAGCCATTACAGTATCTGTGAG 915

RESULT 2
US-10-158-895-14
; Sequence 14, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1776)
US-10-158-895-14

Alignment Scores:
Pred. No.: 9,04e-146
Score: 1252.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x US-10-158-895-14 (1-1788)

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Db 232 GTAGACCTTCGGCAGTTATCCCGTGAACCAATCTTAATATTGTAAAGCTTTATGAGCC 291
QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40
Db 292 TCGTTGAATCCAGTGTCTTGTGATGAAATATGCGAAGGGGGCTCTTTATATATATG 351
QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
Db 352 CTGCATGTGTGTAACCATTCATATATATCTGCTGCCCAAGCAATGAGTTGGTTT 411
QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProValAlaLeuIleHisArg 80
Db 412 CAGTGTTCACAGAGAGTGGCTTATCTTCACAGCAAGCAACCAAGCGCTAATTCACAG 471
QY 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuValIleCysAsp 100
Db 472 GACCTGAACCAACCAACTTACTGCTGGTGCAGGGGGGCAAGTTCTTAAATAATTTGAT 531
QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 120
Db 532 TTGGGTACAGCCTGTGAATTCACACACATGACCAATTAACAAGGGAGTGTGCTGG 591
QY 121 MetAlaProGluValPheGlyGlySerAsnTyrSerGluLysCysAspValPheSerTyr 140
Db 592 ATGGACCTGAAGTTTGAAGTATGATTAACATGTAATAATGTAAGTGTGCTGG 651
QY 141 GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyPro 160
Db 652 GGTATATATCTTGTGGAGATGATACGGTGCAGAAACCTTTGATGATGGTGGCCCA 711
QY 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProPheLeuIleValAsnLeu 180
Db 712 GCTTTCGAAATCAGTGTGGCTGTCTCATATATGATCTGCAGCACCATGATTAATAATTTA 771
QY 181 ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 200
Db 772 CCTAAGCCCATGTGAGACCTGATGACTCGTGTGGCTTAAAGATCTTCCAGGCCCT 831
QY 201 SerMetGluGluIleValIleValIleMetThrHisLeuMetLysGlyPheProGlyAlaAsp 220
Db 832 TCATATGAGAAATTTGTGAATAATATGACTCACTTATGCGTACTTTCCAGAGCAGAT 891
QY 221 GluProLeuGlnTyrProCysGln 228
Db 892 GAGCCATTACAGTATCTGTGAG 915

RESULT 3
US-08-685-625A-5
; Sequence 5, Application US/08685625A
; Patent No. 5945301
; GENERAL INFORMATION:
; APPLICANT: UENO, Naoto
; APPLICANT: MATSUMOTO, Kunhiro
; APPLICANT: IRIE, Kenji
; TITLE OF INVENTION: NOVEL KINASE IN TGF-BETA FAMILY SIGNAL TRANSDUCTION SYSTEM

```

NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,625A  
FILING DATE: 24-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-253549  
FILING DATE: 29-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 001560-267  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2656 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 183..1922  
US-08-685-625A-5  
Alignment Scores:  
Pred. No.: 1,68e-145 Length: 2656  
Score: 1252.00 Matches: 228  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 2  
US-09-830-144-2\_COPY\_76\_303 (1-228) x US-08-685-625A-5 (1-2656)  
QY 1 ValGluLeuAArgGlnLeuSerArgValAsnHisProAsnIleValIleLeuTyrGlyAla 20  
DB 408 GTAGAGCTTCGGAGGTATCCCGTGTGAACCATCTTAATATGTAAAGCTTATGAGACC 467  
QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40  
DB 468 TGCCTGAATCCAGTGTGCTGTGTGATGAAATATGCTGAAGGGGGCTCTTTATATATG 527  
QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60  
DB 528 CTGATGCTGCTGAACCATTCGCAATATATCTGCTGCCAAGCATAGATTGGGTGTTA 587  
QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProValAlaLeuIleHisArg 80  
DB 588 CAGTGTCCCAAGAGAGGTCTTATCTTCAAGCAGCAACCCAAAGCGCTAATTCACAGG 647  
QY 81 AspleuAspProProAsnLeuLeuValAlaGlyGlyThrValLeuIleGlyCysAsp 100  
DB 648 GACCTGAACCAACCAACTTACTGCTGTGTCAGAGGGGGAGCAAGTTCTAAATTTGTGAT 707  
QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetTyrAsnAsnIleGlySerAlaAlaTyr 120  
DB 708 TTGCTACAGCTGTGATCTTCAAGACACACATGACCAATATACAAAGGGAGGTGCTGCTGG 767

QY 121 MetAlaProGluValPheGlySerAsnTyrSerGluIleCysAspValPheSerTyr 140  
DB 768 ATGGACCTGTAAGTTTGAAGGTATTAATTAACAGTAAAGTGAAGTGCCTTCAGCTGG 827  
QY 141 GlyIleIleLeuTyrGluValIleThrArgArgLeuPheAspGluIleGlyGlyPro 160  
DB 828 GGTATATTTCTTGGGAAAGATTAACCGCTGGAAACCTTTGATGATGGAGGCCCA 887  
QY 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleIleAsnLeu 180  
DB 888 GCTTCCGAATCATGTGGCTGTTCATATAGTACTGACACACCATCATTAATAATTTA 947  
QY 181 ProIleProIleGluSerLeuMetThrArgCysTyrSerIleAspProSerGlnArgPro 200  
DB 948 CTTAGGCCCATTTGAGACCTGATGACTGTTGTGTGCTAAAGATCCTTCCAGAGCCCT 1007  
QY 201 SerMetGluGluIleValIleGlyIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220  
DB 1008 TCATGAGAGAAATTTGAAATATATGACTTATGATGGGTACTTTCCAGAGCAGAT 1067  
QY 221 GluProLeuGlnTyrProCysGln 228  
DB 1068 GAGCCATTACGATATCCTTGTCAG 1091  
RESULT 4  
US-09-529-279-3  
Sequence 3, Application US/09529279  
Patent No. 645167  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT FILING DATE: US/09/529, 279  
PRIOR FILING DATE: 2000-04-11  
CURRENT FILING DATE: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48.  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 2656  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (183)..(1919)  
US-09-529-279-3  
Alignment Scores:  
Pred. No.: 1,68e-145 Length: 2656  
Score: 1252.00 Matches: 228  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 3  
US-09-830-144-2\_COPY\_76\_303 (1-228) x US-09-529-279-3 (1-2656)  
QY 1 ValGluLeuAArgGlnLeuSerArgValAsnHisProAsnIleValIleLeuTyrGlyAla 20  
DB 408 GTAGAGCTTCGGAGGTATCCCGTGTGAACCATCTTAATATGTAAAGCTTATGAGACC 467  
QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40  
DB 468 TGCCTGAATCCAGTGTGCTGTGTGATGAAATATGCTGAAGGGGGCTCTTTATATATG 527  
QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60  
DB 528 CTGATGCTGCTGAACCATTCGCAATATATCTGCTGCCAAGCATAGATTGGGTGTTA 587



```

QY      61  GlnCysSerGlnGlyValAlaIleuHisSerMetGlnProIleuAlaIleuHisArg 80
DB      588  CAGTGTTCACAGAGAGGCTTATCTTCACAGCATCAACCCAAAGCGCTAATTCACAGG 647
QY      81  AspLeuLysProProAsnLeuLeuValAlaGlyIleuValLeuLysIleuLysAsp 100
DB      648  GACCTGAACCAACCAACTTACTGCTGCTTGCGAGGGGAGACAGTCTAATAAATTTGTAT 707
QY      101  PheGlyThrAlaCysAspIleuIleuThrHisMetThrAsnAsnLysGlySerAlaIleu 120
DB      708  TTGTGTACAGCCCTGTACATTCAGACACATGACCAATTAACAAGGAGAGTCTGCTGG 767
QY      121  MetAlaProGluValPheGluGlySerAsnLysSerGluLysCysAspValPheSerTrp 140
DB      768  ATGGACACCTGAAGTTTATTAAGTACTATTAACAGTAAATGAGAGTCTTCAGCTGG 827
QY      141  GlyIleIleuTrpGluValIleuThrArgArgLysProPheAspGluIleuGlyPro 160
DB      828  GGTATTATCTTTGGAGAGTGAACGCGTCGGAACCTTTGATGAGATTGGTGCCCA 887
QY      161  AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProIleuIleuLysAsnLeu 180
DB      888  GCTTCCCAATCATGTGGCTGTCTCATATAGTACTGACCACTGATATAAATTTTA 947
QY      181  ProLysProIleuGlySerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200
DB      948  CCTAAGCCCATGAGAGCGCTGACTGCTGTGCTAAGATCCTTCCAGAGCCCT 1007
QY      201  SerMetGluGluIleValLysIleuMetThrHisLeuMetArgLysPheProGlyAlaAsp 220
DB      1008  TCAATGAGAGAAATTTGAAATATATGACTCACTTGATGCGGTACTTCCAGAGCAGAT 1067
QY      221  GluProLeuGlnLysProCysGln 228
DB      1068  GAGCATTAAGATCCTTGTCTGAG 1091

```

## RESULT 5

```

US-10-158-895-3
; Sequence 3, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHITAKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158, 895
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529, 279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2656
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (183)...(1919)
US-10-158-895-3

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## Alignment Scores:

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Pred. No.: 1,68e-145
Score: 1252.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4

```

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Length: 2656
Matches: 228
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

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US-09-830-144-2\_copy\_76\_303 (1-228) x US-10-158-895-3 (1-2656)

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QY      1  ValGluLeuArgGlnLeuSerArgValAlaHisProAsnIleValLysLeuTrpGlyAla 20
DB      408  GTAGAGCTTGCGGAGATATCCGCTGGAACCATCTTAATATTTGTAAGCTTTATGAGGCC 467
QY      21  CysLeuAsnProValCysLeuValMetGluTrpAlaGluGlyLysSerLeuTrpAsnVal 40
DB      468  TGCCTGATTCAGTGTGTCTTGATGATGATATGCTGAAGGGGGCTCTTATATATATG 527
QY      41  LeuHisGlyAlaGluProLeuProLysTrpTrpAlaAlaHisAlaMetSerTrpCysLeu 60
DB      528  CTGCATGCTGTGAACCAATTGCAATATATATGCTGCGCCAGCAATGATGAGTTTA 587
QY      61  GlnCysSerGlnGlyValAlaIleuHisSerMetGlnProLysAlaIleuHisArg 80
DB      588  CAGTGTTCACAGAGAGTGTCTTATCTTCACAGCATCAACCCAAAGCGCTAATTCACAGG 647
QY      81  AspLeuLysProProAsnLeuLeuValAlaGlyIleuValLeuLysIleuLysAsp 100
DB      648  GACCTGAACCAACCAACTTACTGCTGCTGAGGGGAGACAGTCTAATAAATTTGTAT 707
QY      101  PheGlyThrAlaCysAspIleuIleuThrHisMetThrAsnAsnLysGlySerAlaIleu 120
DB      708  TTGTGTACAGCCCTGTACATTCAGACACATGACCAATTAACAAGGAGAGTCTGCTGG 767
QY      121  MetAlaProGluValPheGluGlySerAsnLysSerGluLysCysAspValPheSerTrp 140
DB      768  ATGGACACCTGAAGTTTATTAAGTACTATTAACAGTAAATGAGAGTCTTCAGCTGG 827
QY      141  GlyIleIleuTrpGluValIleuThrArgArgLysProPheAspGluIleuGlyPro 160
DB      828  GGTATTATCTTTGGAGAGTGAATACGCGTCGGAACCTTTGATGAGATTGGTGCCCA 887
QY      161  AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProIleuIleuLysAsnLeu 180
DB      888  GCTTCCCAATCATGTGGCTGTCTCATATAGTACTGACCACTGATATAAATTTTA 947
QY      181  ProLysProIleuGlySerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200
DB      948  CCTAAGCCCATGAGAGCGCTGACTGCTGTGCTAAGATCCTTCCAGAGCCCT 1007
QY      201  SerMetGluGluIleValLysIleuMetThrHisLeuMetArgLysPheProGlyAlaAsp 220
DB      1008  TCAATGAGAGAAATTTGAAATATATGACTCACTTGATGCGGTACTTCCAGAGCAGAT 1067
QY      221  GluProLeuGlnLysProCysGln 228
DB      1068  GAGCATTAAGATCCTTGTCTGAG 1091

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## RESULT 6

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US-09-949-016-4031
; Sequence 4031, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4031
; LENGTH: 2769
; TYPE: DNA
; ORGANISM: Human

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US-09-949-016-4031

Alignment Scores:

Pred. No.:	Length:	Matches:
1,79e-145	2769	1252.00
Score:		228
Percent Similarity:		100.00%
Best Local Similarity:		100.00%
Query Match:		100.00%
DB:		

US-09-830-144-2\_COPY\_76\_303 (1-228) x US-09-949-016-4031 (1-2769)

QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIysLeuTyGlyAla 20  
 DB 388 GTAGAGCTTCGGCAGTTATCCCGTGAACCATCTTATATTGTAAGCTTATGAGCC 447  
 QY 21 CysLeuAsnProValCysLeuValMetGluTyRAlaGluGlyGlySerLeuTyAsnVal 40  
 DB 448 TGCTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTATATATATGTG 507  
 QY 41 LeuHisGlyAlaGluProLeuProTyTyThrAlaAlaHisAlaMetSerTyCysLeu 60  
 DB 508 CTGATGTGTCTGAACCATTCCTATATATCTGCTGCCACGCAATGAGTGTGTTTA 567  
 QY 61 GluCysSerGlnGlyValAlaTyRLeuHisSerMetGlnProIysAlaLeuIleHisArg 80  
 DB 568 CAGGTTCCTCCAGAGAGTGTATCTTATCTTCAAGATGCAACCAAGGCTTATTCACAGG 627  
 QY 81 AspleuIysProProAsnLeuLeuValAlaGlyGlyTyRValLeuIysIleCysAsp 100  
 DB 628 GACCTGAACCAACCAATTAATCTGCTGTGTCAGGGGGGACAGTCTTAAATTTGGAT 687  
 QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnIysGlySerAlaAlaTrp 120  
 DB 688 TTGCTGACAGCTGTGACATTCAGACACATGACCAATATCAAGGGGAGTGTGCTTGG 747  
 QY 121 MetAlaProGluValPheGluGlySerAsnTyRSerGlyIysCysAspValPheSerTrp 140  
 DB 748 ATGGCACCCTGAAGTTTGAAGTAGTATTAAGTGAATGAATGACGTCTTCACGCTGG 807  
 QY 141 GlyIleIleLeuTyRGlulValIleThrArgArgIysProPheAspGluIleGlyIysPro 160  
 DB 808 GGTATTATCTTGTGGAGATGATTAACGGCTGCAAACTTGTATGATGTGTGGCCCA 867  
 QY 161 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleIysAsnLeu 180  
 DB 868 GCTTCGAATCATGTGGCTGTTCATATGTACTCCACCACTATATAAAATTTTA 927  
 QY 181 ProIysProIleGluSerLeuMetThrArgCysTrpSerIysAspProSerGluArgPro 200  
 DB 928 CCTAAGCCCATGAGAGCTGATGATCGTGTGTGTTAAAGATCTTCCACAGGCCCT 987  
 QY 201 SerMetGluGluIleValIysIleMetThrHisLeuMetArgTyRPhProGlyAlaAsp 220  
 DB 988 TCAATGAGGAATTTGAAATATATGACTCACTTGATGCGGTACTTTCAGAGACAGAT 1047  
 QY 221 GluProLeuGlnTyRProCysGln 228  
 DB 1048 GAGCATTTACAGTATCTTGTGAG 1071

RESULT 7

US-08-685-625A-1

Sequence 1, Application US/08685625A

Patent No. 5945301

GENERAL INFORMATION:

APPLICANT: UENO, Naoto

APPLICANT: MATSUMOTO, Kunihito

APPLICANT: IRIE, Kenji

TITLE OF INVENTION: NOVEL KINASE IN TGF-BETA FAMILY SIGNAL

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSER: BURNS, DOANE, SWECKER &amp; MATHIS, L.L.P.

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/685,625A

FILING DATE: 24-JUL-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-253549

FILING DATE: 29-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: Meuth, Donna M.

REGISTRATION NUMBER: 36,607

REFERENCE/DOCKET NUMBER: 001560-267

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2443 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 157..1893

US-08-685-625A-1

Alignment Scores:

Pred. No.:	Length:	Matches:
6.2e-145	2443	1247.00
Score:		227
Percent Similarity:		100.00%
Best Local Similarity:		100.00%
Query Match:		99.60%
DB:		

US-09-830-144-2\_COPY\_76\_303 (1-228) x US-08-685-625A-1 (1-2443)

QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIysLeuTyGlyAla 20  
 DB 382 GTGAGGCTCCGGCAGTTGTGCGTGTGAACCATCTTAACTGTCAAGTGTACGAGCC 441  
 QY 21 CysLeuAsnProValCysLeuValMetGluTyRAlaGluGlyGlySerLeuTyAsnVal 40  
 DB 442 TGCTGAATCCAGTGTCTTGTGATGGAATATGACAGGGGGCTCATTTATATATGTG 501  
 QY 41 LeuHisGlyAlaGluProLeuProTyTyThrAlaAlaHisAlaMetSerTyCysLeu 60  
 DB 502 CTGATGTGTCTGAACCATTCCTTACACCTGCTCTCAAGCATGACTGTGTTTA 561  
 QY 61 GluCysSerGlnGlyValAlaTyRLeuHisSerMetGlnProIysAlaLeuIleHisArg 80  
 DB 562 CAGTGTTCCTCCAGAGAGTGTCTTACCTGCAAGATGCAAGCCCAAGCGCTGATTCACAGG 621  
 QY 81 AspleuIysProProAsnLeuLeuValAlaGlyGlyTyRValLeuIysIleCysAsp 100  
 DB 622 GACCTCAAGCTCCCAATCTTCTGTGTTCCAGAGGAGACAGTCTTAAATCTGCAT 681  
 QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnIysGlySerAlaAlaTrp 120  
 DB 682 TTGCTGACAGCTTGTGATCAACCAACATGACCAATATTAAGAGAGTCTGCTGG 741  
 QY 121 MetAlaProGluValPheGluGlySerAsnTyRSerGlyIysCysAspValPheSerTrp 140  
 DB 742 ATGGGCTGAGAGTGTGGAAGTAGCAATTAACAGTGAAGAGTGTGATGTCTTCAAGCTGG 801

```
QY 141 GYIlelleleuptrpGluValIlethArgArgLyseProPheaspGluIleGlyGlyPro 160
Db 802 GGATTAATATCTCTGGAGAGATGATACACCGCGGAACCTTGATGATGATCGTGCCCA 861
QY 161 AlAphaArgIleMetThrAlaValHisamGlyThArgProProleuIleLysAsnLeu 180
Db 862 GCTTTAGATATCATGAGGGGTGTTCAATATGACACACCACTGATCAAAATTTTA 921
QY 181 ProLysProIleGluSerLeuMetThrArgCysTTPSerLysAspProSerGlnArgPro 200
Db 922 CCAAGCCCATGAGAGCTGATGACACCGCTGTGTCAGAACCCATCTCAGGCCCTT 981
QY 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
Db 982 TCAATGAGAGAAATGTGAAATAATGACTCATTTGATGCGGTACTTCCAGAGCGGAT 1041
QY 221 GluProLeuGlnTyrProCys 227
Db 1042 GAGCCATTACAGTATCTTGT 1062

RESULT 8
US-09-949-016-1327
; Sequence 1327, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1327
; LENGTH: 3143
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1327

Alignment Scores:
Pred. No.: 3,498-38 Length: 3143
Score: 392.50 Matches: 88
Percent Similarity: 56.68% Conservative: 35
Best Local Similarity: 40.55% Mismatches: 77
Query Match: 31.35% Indels: 17
Gaps: 6

US-09-830-144-2_COPY_76_303 (1-228) x US-09-949-016-1327 (1-3143)
QY 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAlaCys 21
Db 594 GAAGCCCGGCTCTTTGAGCCCTGAGCCGCCCAACATATGAGCTTGGAGGCGCTGCG 653
QY 22 LeuAsnPro-----ValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn 39
Db 654 CTCACACCCCAACACACTCTGCTAGTGAATGAGATATGCCGGGGTGGTGCACCTAGACAGG 713
QY 40 ValLeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCys 59
Db 714 GAGCTGGACAGGTGCGCGGGTGCACCTCACTG-----CTGGTCAACTGGGCT 761
QY 60 LeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHis 79
Db 762 GTCGAGAGTGGCGCGGGGATGAATACCTACACAAATGATGCCCTGTGCCATCATCAAC 821
QY 80 ArgAspLeuLysProProAsnLeuLeuVal-----AlaGly 92
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Db 822 CGGAGCTCAAGTCCATCAATCAATCTGATCTGGAGGCCATGAGAACCAACACTCGCA 881
QY 93 GlyThrValLeuLysIleCysAspPheGlyThrAlaCysAsp---IleGlnThrHisMet 111
Db 882 GACACGGTGTCTCAAGATCAAGATCGAGCTTGGCTCGCCCGGAGTGGACAAAGCCAG 941
QY 112 ThrAsnAsnLysGlySerAlaAlaTyrMetAlaProGluValPheGluGlySerAsnTyr 131
Db 942 ATGAGGCTGGCGGGGACTTACAGCTTGATGCGCGGAGATTAATCGTCTCCCTTC 1001
QY 132 SerGluLysCysAspAlaPheSerTyrGlyIleLeuThrGluValIleThrArgArg 151
Db 1002 TCCAAAAGACATGATTCGAGAGCTTGGAGCTGCTGTGGAGACTCTGACGGGGAG 1061
QY 152 LysProPheAspGluIleGlyGlyProAlaPheArgIleMetThrAlaVal---HisAsn 170
Db 1062 GTCCCTTACCGTAGATC-----GACGCTTGGCGCGTATGAGGCTATGAGCTATGAT 1115
QY 171 GlyThrArgProProleuIleLysAsnLeuProLysProIleGluSerLeuMetThrArg 190
Db 1116 MAGCTAGCGCTGCCATTCCTTCCACGTGCGCCGAGCCCTTGGCCGCTCTCGAGGAA 1175
QY 191 CysTTPSerLysAspProSerGlnArgProSerMetGluGluIleValLys 207
Db 1176 TCTGGGACCCAGACCCCAAGGGCGGCGGAGATTTGGTATGATCTTGAAG 1226

RESULT 9
US-09-221-235-6
; Sequence 6, Application US/09221235
; Patent No. 6043040
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MN1-050
; CURRENT APPLICATION NUMBER: US/09/221,235
; PRIOR FILING DATE: 1998-12-28
; EARLIER FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1365)
US-09-221-235-6

Alignment Scores:
Pred. No.: 4,538-36 Length: 1365
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
Gaps: 8

US-09-830-144-2_COPY_76_303 (1-228) x US-09-221-235-6 (1-1365)
QY 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAlaCys 21
Db 157 GAGGCAAGAAATATCATGTTCTCTCACTGTCACAAACATATCATCAAGTTTATGAGATTAAT 216
QY 22 LeuAsnPro-----ValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn 39
Db 217 CTGAACTCTCCCAACATATGAGTGTGCAGAAATATGCTTCTCTGGATCACTCATATAT 276
QY 40 ValLeuHisGly-----AlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSer 57
Db 277 TACATTAAACAGTAACAGAAAGTAGAGATG-----GATATGATGATCAATTAATAGCC 327
QY 58 TrpCysLeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeu 77
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Db 328 TGGGCCACTGATGTAGCCAAAGAAATGATATTATTAATGAGAGCTCCCTGTCAGAGTG 387  
Qy 78 TLehiSaRgApLeuLyProProAsnLeuLeuValAlaGlyGlyThrValLeuLy 97  
Db 388 ATTCAAGAGAACCTCAAGTCAAGAAACGTTGTATTAAGCTGCTGATGGA---GTACTGAAG 444  
Qy 98 TLeCySaRgPheGlyThrAlaCySaRgPLeGlnThrHisMetThrAsnLeuLy----- 115  
Db 445 ATCTGATCACTTGGT---GCCCTCGGTTCCATACCAATACACACACATGCTCTTGTT 501  
Qy 116 GlySerAlaAlaTrpMetAlaProGluValPheGluGlySerAsnTrpSerGluLyCyS 135  
Db 502 GGAACCTTCCCAAGAGAGTCCCGCAAGATTAATCAAGAGTCCCTGATGTCAGAAACTGT 561  
Qy 136 AspValPheSerTrpGlyIleLeuTrpGluValIleThrArgArgLyProPheAsp 155  
Db 562 GACACATATTCCTATGCTGTGCTCTGGAAGATGCTAACAGAGGAGTCCCTTTAAA 621  
Qy 156 GluIleGlyGlyProAlaPheArgIleMetTrp---AlaValHisAsnGlyThrArgPro 174  
Db 622 GGTTCGAGAGA-----TTACAAGTAGCTTGCTGTAGTGAAGAAAAACGAGAGATTA 675  
Qy 175 ProLeuIleLySaLeuLeuProLyProIleGluSerLeuMetThrArgCySTrpSerLyS 194  
Db 676 ACCATTCCAAAGCAAGTTCGCCCAAGAGTTTGTCTGAACGTTCATCACTGTTGGAGAGCT 735  
Qy 195 AspProSerGlnArgProSerMetGluGluIleValLySileMet 209  
Db 736 GATCCCAAGAAACGCGCATCATTCACAGCAATCATTCATTCCTG 780  
RESULT 10  
US-09-221-928-6  
; Sequence 6, Application US/09221928  
; Patent No. 6121030  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan  
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
; FILE REFERENCE: NMI-050  
; CURRENT APPLICATION NUMBER: US/09/221,928  
; EARLIER FILING DATE: 1998-12-28  
; EARLIER APPLICATION NUMBER: 09/163,115  
; EARLIER FILING DATE:  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1365  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1365)  
US-09-221-928-6  
Alignment Scores:  
Pred. No.: 4.53e-36 Length: 1365  
Score: 371.00 Matches: 81  
Percent Similarity: 56.28% Conservative: 40  
Best Local Similarity: 37.67% Mismatches: 80  
Query Match: 29.63% Indels: 14  
DB: 3 Gaps: 8  
US-09-830-144-2\_COPY\_76\_303 (1-228) x US-09-221-928-6 (1-1365)  
Qy 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLyLeuTrpGlyValaCys 21  
Db 157 GAGGAGAAATTAATCTAGTCTCTCACTCAACAGAAACATATCCATTTTATGAGATTA 216  
Qy 22 LeuAsnPro-----ValCyLeuValMetGluTrpAlaGluGlyGlySerLeuTrpAsn 39  
Db 217 CTTGAACCTCCCACTATGTCATGTGTCAAGAAATATGCTTCTGTGGATCACTTATGAT 276  
Qy 40 ValLeuHisGly-----AlaGluProLeuProLyTrpThrAlaHisIleMetSer 57

Db 277 TACATTAAACAGTAACAGAGTGAAGAGATG-----GATATGATCACTTATTAACC 327  
Qy 58 TrpCyLeuGlnCySerGlnGlyValAlaTyLeuHisSerMetGlnProLySaLeu 77  
Db 328 TGGGCCACTGATGTAGCCAAAGAAATGATATTATTAATGAGAGCTCCCTGTCAGAGTG 387  
Qy 78 TLehiSaRgApLeuLyProProAsnLeuLeuValAlaGlyGlyThrValLeuLy 97  
Db 388 ATTCAAGAGAACCTCAAGTCAAGAAACGTTGTATTAAGCTGCTGATGGA---GTACTGAAG 444  
Qy 98 TLeCySaRgPheGlyThrAlaCySaRgPLeGlnThrHisMetThrAsnLeuLy----- 115  
Db 445 ATCTGATCACTTGGT---GCCCTCGGTTCCATACCAATACACACACATGCTCTTGTT 501  
Qy 116 GlySerAlaAlaTrpMetAlaProGluValPheGluGlySerAsnTrpSerGluLyCyS 135  
Db 502 GGAACCTTCCCAAGAGAGTCCCGCAAGATTAATCAAGAGTCCCTGATGTCAGAAACTGT 561  
Qy 136 AspValPheSerTrpGlyIleLeuTrpGluValIleThrArgArgLyProPheAsp 155  
Db 562 GACACATATTCCTATGCTGTGCTCTGGAAGATGCTAACAGAGGAGTCCCTTTAAA 621  
Qy 156 GluIleGlyGlyProAlaPheArgIleMetTrp---AlaValHisAsnGlyThrArgPro 174  
Db 622 GGTTCGAGAGA-----TTACAAGTAGCTTGCTGTAGTGAAGAAAAACGAGAGATTA 675  
Qy 175 ProLeuIleLySaLeuLeuProLyProIleGluSerLeuMetThrArgCySTrpSerLyS 194  
Db 676 ACCATTCCAAAGCAAGTTCGCCCAAGAGTTTGTCTGAACGTTCATCACTGTTGGAGAGCT 735  
Qy 195 AspProSerGlnArgProSerMetGluGluIleValLySileMet 209  
Db 736 GATCCCAAGAAACGCGCATCATTCACAGCAATCATTCATTCCTG 780  
RESULT 11  
US-09-221-527-6  
; Sequence 6, Application US/09221527  
; Patent No. 6146832  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan  
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
; FILE REFERENCE: NMI-050  
; CURRENT APPLICATION NUMBER: US/09/221,527  
; EARLIER FILING DATE: 1998-12-28  
; EARLIER APPLICATION NUMBER: 09/163,115  
; EARLIER FILING DATE:  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1365  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1365)  
US-09-221-527-6  
Alignment Scores:  
Pred. No.: 4.53e-36 Length: 1365  
Score: 371.00 Matches: 81  
Percent Similarity: 56.28% Conservative: 40  
Best Local Similarity: 37.67% Mismatches: 80  
Query Match: 29.63% Indels: 14  
DB: 3 Gaps: 8  
US-09-830-144-2\_COPY\_76\_303 (1-228) x US-09-221-527-6 (1-1365)  
Qy 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLyLeuTrpGlyValaCys 21  
Db 157 GAGGAGAAATTAATCTAGTCTCTCACTCAACAGAAACATATCCATTTTATGAGATTA 216  
Qy 22 LeuAsnPro-----ValCyLeuValMetGluTrpAlaGluGlyGlySerLeuTrpAsn 39

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Db 217 CTTGAACCTCCCAACTATGTCATGTCACAGAAATGCTTCTGCGATCACTATGAT 276
Qy 40 ValLeuHieglY-----AlaGluProLeuProYrYrThrAlaAlaHieglY 57
Db 277 TACATTAAAGTAACAGAGATGAGAGATG-----GATATGATATCACTTATGACC 327
Qy 58 TrpCysLeuGlnCysSerGlnGlyValAlaYrLeuHieglYsSerMetGlnProYsAlaLeu 77
Db 328 TGGGCCACTGATGATGACCAAGAAATGCAATTATTAATGATGAGAGCTCTGTCAGAGTG 387
Qy 78 IleHieAspLeuLeuProProLeuLeuLeuValAlaGlyYrThrValLeuYs 97
Db 388 ATTCACAGAGACCTCAAGTCAGAAACGTTTATATAGCTGCTGATGAG---GTACTGAG 444
Qy 98 IleCysAspPheGlyThrAlaCysAspIleGlnThrHieMetThraAsnLys----- 115
Db 445 ATCTGTGACTTTGGT---GCTCTGCTGCTTCCATTAACATCAACACACATGCTTGGTT 501
Qy 116 GlySerAlaAlaTrpMetAlaProGluValPheGluGlySerAsnYrSerGluYsCys 135
Db 502 GGAACCTTCCCATGATGATGCTCCAGAAAGTTATCCAGAGTCCTCCCTGTGAGAACTGT 561
Qy 136 AspValPheSerTrpGlyIleIleLeuTrpGluValIleThrArgArgLysProPheAsp 155
Db 562 GACACATATCTCTATGATGATGCTTCTGAGAGATGCTAACAGAGAGCTCCCTTAAA 621
Qy 156 GluIleGlyProAlaPheArgIleMetTrp---AlaValHieAsnGlyThraArgPro 174
Db 622 GGTTCGAGAGG-----TTACAAGTAGCTTGGCTTGAAGTGAAGAAACGAGAGATTA 675
Qy 175 ProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThraArgYsTrpSerLys 194
Db 676 ACCATTCACAGACAGTTCGCCAGAAAGTTTGTCTGAAGCTGTATCAATCATGTTGGAAGCT 735
Qy 195 AspProSerGlnArgProSerMetGluGluIleValYsIleMet 209
Db 736 GATGCCAAGAAACGGCCATCTTCAAGCAATCATTTCAATCTCG 780
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## RESULT 12

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US-09-221-236-6
; Sequence 6, Application US/09221236
; Patent No. 6146841
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: NMI-050
; CURRENT APPLICATION NUMBER: US/09/221,236
; EARLIER FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-221-236-6
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## Alignment Scores:

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Pred. No.: 4,53e-36 Length: 1365
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: Gaps: 8
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US-09-830-144-2\_COPY\_76\_303 (1-228) x US-09-221-236-6 (1-1365)

Qy 2 GluLeuArgGlnLeuSerArgValAsnHisProLeuIleValLysLeuTrpGlyValaCys 21

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Db 157 GAGCGAAGAAATACCTAGCTGTCTCAGTCACAGAAATCATCTCAGTTTATGAGTAATT 216
Qy 22 LeuAsnPro-----ValCysLeuValMetGluYrAlaGluGlyYsSerLeuYrAsn 39
Db 217 CTTGAACCTCCCAACTATGTCATGTCACAGAAATGCTTCTGCGATCACTATGAT 276
Qy 40 ValLeuHieglY-----AlaGluProLeuProYrYrThrAlaAlaHieglY 57
Db 277 TACATTAAAGTAACAGAGATGAGAGATG-----GATATGATATCACTTATGACC 327
Qy 58 TrpCysLeuGlnCysSerGlnGlyValAlaYrLeuHieglYsSerMetGlnProYsAlaLeu 77
Db 328 TGGGCCACTGATGATGACCAAGAAATGCAATTATTAATGATGAGAGCTCTGTCAGAGTG 387
Qy 78 IleHieAspLeuLeuProProLeuLeuLeuValAlaGlyYrThrValLeuYs 97
Db 388 ATTCACAGAGACCTCAAGTCAGAAACGTTTATATAGCTGCTGATGAG---GTACTGAG 444
Qy 98 IleCysAspPheGlyThrAlaCysAspIleGlnThrHieMetThraAsnLys----- 115
Db 445 ATCTGTGACTTTGGT---GCTCTGCTGCTTCCATTAACATCAACACACATGCTTGGTT 501
Qy 116 GlySerAlaAlaTrpMetAlaProGluValPheGluGlySerAsnYrSerGluYsCys 135
Db 502 GGAACCTTCCCATGATGATGCTCCAGAAAGTTATCCAGAGTCCTCCCTGTGAGAACTGT 561
Qy 136 AspValPheSerTrpGlyIleIleLeuTrpGluValIleThrArgArgLysProPheAsp 155
Db 562 GACACATATCTCTATGATGATGCTTCTGAGAGATGCTAACAGAGAGCTCCCTTAAA 621
Qy 156 GluIleGlyProAlaPheArgIleMetTrp---AlaValHieAsnGlyThraArgPro 174
Db 622 GGTTCGAGAGG-----TTACAAGTAGCTTGGCTTGAAGTGAAGAAACGAGAGATTA 675
Qy 175 ProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThraArgYsTrpSerLys 194
Db 676 ACCATTCACAGACAGTTCGCCAGAAAGTTTGTCTGAAGCTGTATCAATCATGTTGGAAGCT 735
Qy 195 AspProSerGlnArgProSerMetGluGluIleValYsIleMet 209
Db 736 GATGCCAAGAAACGGCCATCTTCAAGCAATCATTTCAATCTCG 780
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## RESULT 13

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US-09-221-416-6
; Sequence 6, Application US/09221416
; Patent No. 6153417
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: NMI-050
; CURRENT APPLICATION NUMBER: US/09/221,416
; EARLIER FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-221-416-6
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## Alignment Scores:

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Pred. No.: 4,53e-36 Length: 1365
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: Gaps: 8
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US-09-830-144-2\_COPY\_76\_303 (1-228) x US-09-221-416-6 (1-1365)

QY 2 GluLeuArgLInLeuSerArgValAsnHisProAsnIleValIysLeuTYRGIYValaCys 21  
 157 GAGGCAGAAATATCTCAAGTCTCCAGTCAAGAAATCAATCCAGTTTATGGAGTATT 216  
 Db 22 LeuAsnPro-----ValCysLeuValMetGluTYRValaGluGlyGlySerLeuTYRAsn 39  
 217 CTGGAACCTCCCAACTATGAGCATTTGCTCAAGAAATATGCTCTCGGAGATCACTTATGAT 276  
 QY 40 ValLeuHisGly-----AlaGluProLeuProTYRThrAlaAlaHisAlaMetSer 57  
 277 TACATTACAGTAACAGAAAGTGAAGATG-----GATATGATCACTATATAC 327  
 Db 58 TrpCysLeuGlnCysSerGlnGlyValAlaTYRLeuHisSerMetGlnProIysAlaLeu 77  
 328 TGGGCCACTGATGATGACCAAGAAATGATATTTATGAGAGGCTCTGTCAGAGTG 387  
 QY 78 IleHisArgAspLeuLysProProAsnLeuLeuValAlaGlyGlyTYRValLeuLys 97  
 388 ATTACAGAGACCTCAAGTCAAGAAAGCTGTGTATAGCTGCTGATGGA--GTACTGAAG 444  
 QY 98 IleCysAspPheGlyTYRAlaCysAspIleGlnThrHisMetThrAsnAsnLys----- 115  
 445 ATCTGTACCTTTGGT---GCCCTCGGTTCCATTAACATCAACACACATGCTCTGGTT 501  
 Db 116 GlySerAlaIatPMeAlaProGluValPheGluGlySerAsnTYRSerGluLysCys 135  
 502 GGAACCTTCCCATGATGAGTCCCAAGATTTATCCAGAGTCCCTGTGTCAGAACTGT 561  
 QY 136 AspValPheSerTPGlyIleIleLeuTYRValIleThrArgArgLysProPheAsp 155  
 562 GACACATATTCCTATGTGTGTCTCTGAGAGATGCTAACAGAGAGAGTCCCTTTTAA 621  
 Db 156 GluIleGlyGlyProAlaPheArgIleMetTrp--AlaValHisAsnGlyThrArgPro 174  
 622 GGTTCGAAGA-----TTACAAGTAGCTTGCTGTAGTGAAGAAAAACAGAGATTA 675  
 QY 175 ProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThrArgCysTrpSerLys 194  
 676 ACCATTCCAGACAGTTCGCCCAAGAGTTTGTGCTGACATGATCACTGCTTGGGAAGCT 735  
 Db 195 AspProSerGlnArgProSerMetGluGluIleValIysIleMet 209  
 736 GATGCCAAGAAACGGCCATTCATCAAGCAATCAATTCATCAATCTG 780  
 QY 195 AspProSerGlnArgProSerMetGluGluIleValIysIleMet 209  
 736 GATGCCAAGAAACGGCCATTCATCAAGCAATCAATTCATCAATCTG 780  
 Db 195 AspProSerGlnArgProSerMetGluGluIleValIysIleMet 209  
 736 GATGCCAAGAAACGGCCATTCATCAAGCAATCAATTCATCAATCTG 780  
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 US-09-221-245-6  
 ; Sequence 6, Application US/09221245  
 ; Patent No. 6180358  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Acton, Susan  
 ; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
 ; FILE REFERENCE: MN-050  
 ; CURRENT APPLICATION NUMBER: US/09/221,245  
 ; CURRENT FILING DATE: 1998-12-28  
 ; EARLIER APPLICATION NUMBER: US 09/163,115  
 ; EARLIER FILING DATE: 1998-09-29  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 6  
 ; LENGTH: 1365  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1365)  
 ; US-09-221-245-6  
 Alignment Scores:  
 Pred. No.: 4,536-36 Length: 1365  
 Score: 371.00 Matches: 81

Percent Similarity: 56.28% Conservative: 40  
 Best Local Similarity: 37.67% Mismatches: 80  
 Query Match: 29.63% Indels: 14  
 DB: 3 Gaps: 8

US-09-830-144-2\_COPY\_76\_303 (1-228) x US-09-221-245-6 (1-1365)

QY 2 GluLeuArgLInLeuSerArgValAsnHisProAsnIleValIysLeuTYRGIYValaCys 21  
 157 GAGGCAGAAATATCTCAAGTCTCCAGTCAAGAAATCAATCCAGTTTATGGAGTATT 216  
 Db 22 LeuAsnPro-----ValCysLeuValMetGluTYRValaGluGlyGlySerLeuTYRAsn 39  
 217 CTGGAACCTCCCAACTATGAGCATTTGCTCAAGAAATATGCTCTCGGAGATCACTTATGAT 276  
 QY 40 ValLeuHisGly-----AlaGluProLeuProTYRThrAlaAlaHisAlaMetSer 57  
 277 TACATTACAGTAACAGAAAGTGAAGATG-----GATATGATCACTATATAC 327  
 Db 58 TrpCysLeuGlnCysSerGlnGlyValAlaTYRLeuHisSerMetGlnProIysAlaLeu 77  
 328 TGGGCCACTGATGATGACCAAGAAATGATATTTATGAGAGGCTCTGTCAGAGTG 387  
 QY 78 IleHisArgAspLeuLysProProAsnLeuLeuValAlaGlyGlyTYRValLeuLys 97  
 388 ATTACAGAGACCTCAAGTCAAGAAAGCTGTGTATAGCTGCTGATGGA--GTACTGAAG 444  
 QY 98 IleCysAspPheGlyTYRAlaCysAspIleGlnThrHisMetThrAsnAsnLys----- 115  
 445 ATCTGTACCTTTGGT---GCCCTCGGTTCCATTAACATCAACACACATGCTCTGGTT 501  
 Db 116 GlySerAlaIatPMeAlaProGluValPheGluGlySerAsnTYRSerGluLysCys 135  
 502 GGAACCTTCCCATGATGAGTCCCAAGATTTATCCAGAGTCCCTGTGTCAGAACTGT 561  
 QY 136 AspValPheSerTPGlyIleIleLeuTYRValIleThrArgArgLysProPheAsp 155  
 562 GACACATATTCCTATGTGTGTCTCTGAGAGATGCTAACAGAGAGAGTCCCTTTTAA 621  
 Db 156 GluIleGlyGlyProAlaPheArgIleMetTrp--AlaValHisAsnGlyThrArgPro 174  
 622 GGTTCGAAGA-----TTACAAGTAGCTTGCTGTAGTGAAGAAAAACAGAGATTA 675  
 QY 175 ProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThrArgCysTrpSerLys 194  
 676 ACCATTCCAGACAGTTCGCCCAAGAGTTTGTGCTGACATGATCACTGCTTGGGAAGCT 735  
 Db 195 AspProSerGlnArgProSerMetGluGluIleValIysIleMet 209  
 736 GATGCCAAGAAACGGCCATTCATCAAGCAATCAATTCATCAATCTG 780  
 QY 195 AspProSerGlnArgProSerMetGluGluIleValIysIleMet 209  
 736 GATGCCAAGAAACGGCCATTCATCAAGCAATCAATTCATCAATCTG 780  
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 736 GATGCCAAGAAACGGCCATTCATCAAGCAATCAATTCATCAATCTG 780  
 RESULT 15  
 US-09-163-115-6  
 ; Sequence 6, Application US/09163115A  
 ; Patent No. 6183962  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Acton, Susan  
 ; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
 ; FILE REFERENCE: MN-050  
 ; CURRENT APPLICATION NUMBER: US/09/163,115A  
 ; CURRENT FILING DATE: 1998-09-29  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 6  
 ; LENGTH: 1365  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1365)  
 ; US-09-163-115-6  
 Alignment Scores:  
 Pred. No.: 4,536-36 Length: 1365  
 Score: 371.00 Matches: 81

Pred. No.: 4,53e-36 Length: 1365  
 Score: 371.00 Matches: 81  
 Percent Similarity: 56.28% Conservative: 40  
 Best Local Similarity: 37.67% Mismatches: 80  
 Query Match: 29.63% Indels: 14  
 DB: 3 Gaps: 8

US-09-830-144-2\_COPY\_76\_303 (1-228) x US-09-163-115-6 (1-1365)

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QY      2  GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIysLeuTyrGlyAlaCys 21
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Db      157  GAGGCAAGAAATATCTCAGTCTCAGTCACAGAAACATCATCCAGTTTATAGAGTAATT 216
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      22  LeuAsnPro-----ValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn 39
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      217  CTTGAACCTCCCAACTATGCAATGCTCAGAAATATGCTTCTCTGGGATCATCTATGAT 276
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      40  ValLeuHisGly-----AlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSer 57
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      277  TACATTAAACAGTAACAGAGTAGAGAGATG-----GATATGATCAGATTATGACC 327
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      58  TyrCysLeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProIysAlaLeu 77
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      328  TGGGCCACTGATGATGACCAAGAGATGATATTATACATATGAGAGCTCCTGTCAGAGTG 387
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      78  IleHisArgAspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLys 97
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      388  ATTACAGAGAGCTTCAAGCTCAAGAAACGTTGTATAGCTGCTGATGGA--GTACTGAAG 444
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QY      98  IleCysAspPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLys-----115
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Db      445  ATCTGTGACTTTGGT--GCCTCTCGGTCCATACCATACATACACACAGATGCTTGTT 501
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      116  GlySerAlaAlaTyrMetAlaProGluValPheGluGlySerAsnTyrSerGluLysCys 135
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      502  GGAACCTTCCATGATGAGCTCCAGAGTTATCCAGAGTCTCCCTGTGTCAAGAACTTGT 561
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      136  AspValPheSerTyrGlyIleIleLeuTyrGluValIleThrArgArgLysProPheAsp 155
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      562  GACACATATCTCTATGCTGTGTTCTCTGGAGATGCTACACAGAGAGTCCCTTTAAA 621
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      156  GluIleGlyGlyProAlaPheArgIleMetTyr--AlaValHisAsnGlyThrArgPro 174
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      622  GGTTTGGAGGA-----TTACAAGTAGCTTGCTGTAGTGGAATAAAGAGAGATTAA 675
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      175  ProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThrArgCysTyrPheLys 194
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      676  ACCATTCCAGAGCGATTGCCAGAGAGTTTGTGAACTGTACATCAGTGTGGGAAGCT 735
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      195  AspProSerGlnArgProSerMetGluGluIleValIysIleMet 209
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      736  GATGCCAAGAAACGGCCATCATTCAGCAAAATCATTTCAATCTCTG 780
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
  
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Search completed: August 2, 2005, 20:47:24  
 Job time : 236.541 secs



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# OM protein - nucleic search, using frame\_plus.p2n model

Run on: August 2, 2005, 20:40:24 ; Search time 845,757 Seconds

(without alignments)  
1744.825 Million cell updates/sec

Title: US-09-830-144-2\_COPY\_76\_303

Perfect score: 1252  
Sequence: 1 VELRQLSRVHNPVIVKLGYA.....MTHLMRYFPADSEPLQYPCQ 226

## Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

-MODEL=frame+ p2n.model -DEV=x1h  
-Q=/cgn2\_1/USPO pool/US09830144/rnat 02082005 101156 12592/app query.fasta\_1.654  
-DB=Published Applications NA -OPMT=fastlap -SUPFIX=p2n.rmpb -MINMATCH=0.1  
-LOOPC=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bloname2  
-TRANS=numan40.cdi -LIST=45 -DOCALLIGN=200 -THR\_SCORE=pcr -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=ptc -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US09830144 @CGN 1 1 1041 @rnat 02082005 101156 12592  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
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- 6: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09C\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
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- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
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- 20: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11A\_NEW\_PUB.seq:\*
- 25: /cgn2\_6/ptodata/1/pubpna/US11A\_NEW\_PUB.seq:\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1252	100.0	1705	14 US-10-283-023-1	Sequence 1, Appl1
2	1252	100.0	1705	14 US-10-283-023-3	Sequence 3, Appl1
3	1252	100.0	1705	17 US-10-386-414-12	Sequence 12, Appl1
4	1252	100.0	1788	13 US-10-158-895-14	Sequence 14, Appl1
5	1252	100.0	1788	16 US-10-384-743-14	Sequence 14, Appl1
6	1252	100.0	2656	13 US-10-158-895-3	Sequence 3, Appl1
7	1252	100.0	2656	16 US-10-384-743-3	Sequence 3, Appl1
8	1252	100.0	2769	18 US-10-343-710-107	Sequence 107, App
9	392.5	31.3	2865	18 US-10-263-929-85	Sequence 85, Appl1
10	392.5	31.3	3138	17 US-10-369-022-55	Sequence 85, Appl1
11	392.5	31.3	3435	16 US-10-210-120-86	Sequence 86, Appl1
12	392.5	31.3	3435	22 US-10-909-035-86	Sequence 86, Appl1
13	392.5	31.3	3454	9 US-09-969-347-226	Sequence 226, App
14	392.5	31.3	3454	15 US-10-171-581-312	Sequence 312, App
15	392.5	31.3	3454	21 US-10-843-641A-8355	Sequence 8355, App
16	387.5	31.0	3476	22 US-10-840-512-109	Sequence 109, App
17	379	30.3	1794	19 US-10-437-963-30121	Sequence 30121, A
18	377	30.1	1540	19 US-10-437-963-73129	Sequence 73129, A
19	374.5	29.9	3238	18 US-10-424-599-129156	Sequence 129156, A
20	373.5	29.8	2327	19 US-10-437-963-54440	Sequence 54440, A
21	373	29.8	1926	18 US-10-425-114-22688	Sequence 22688, A
22	373	29.8	2029	18 US-10-425-114-34394	Sequence 34394, A
23	373	29.8	2091	18 US-10-424-599-110122	Sequence 110122, A
24	373	29.8	2793	20 US-10-425-115-166889	Sequence 166889, A
25	372.5	29.8	3619	18 US-10-112-944-15	Sequence 15, Appl1
26	372.5	29.8	3717	17 US-10-210-130-129	Sequence 129, App
27	372	29.7	1814	18 US-10-425-114-3589	Sequence 3589, App
28	372	29.7	1903	18 US-10-425-114-30893	Sequence 30893, A
29	372	29.7	2106	20 US-10-425-115-166885	Sequence 166885, A
30	371.5	29.7	3092	17 US-10-042-865-15	Sequence 15, Appl1
31	371	29.6	1062	15 US-10-106-698-2068	Sequence 2068, Ap
32	371	29.6	1365	9 US-09-757-982-6	Sequence 6, Appl1
33	371	29.6	1365	21 US-10-786-501-6	Sequence 6, Appl1
34	371	29.6	1718	18 US-10-425-114-11340	Sequence 11340, A
35	371	29.6	2119	18 US-10-352-674A-1	Sequence 1, Appl1
36	371	29.6	2120	9 US-09-757-982-4	Sequence 4, Appl1
37	371	29.6	2120	21 US-10-786-501-4	Sequence 4, Appl1
38	371	29.6	2191	17 US-10-296-115-98	Sequence 98, Appl1
39	371	29.6	2251	17 US-10-094-749-838	Sequence 838, App
40	371	29.6	2455	20 US-10-737-450-65	Sequence 65, Appl1
41	371	29.6	3767	20 US-10-751-736-1	Sequence 1, Appl1
42	370.5	29.6	2207	18 US-10-425-114-22955	Sequence 22955, A
43	370.5	29.6	2866	20 US-10-425-115-36020	Sequence 36020, A
44	370	29.6	1942	18 US-10-425-114-28428	Sequence 28428, A
45	370	29.6	1997	18 US-10-425-114-30767	Sequence 30767, A

## ALIGNMENTS

RESULT 1  
US-10-283-023-1  
Sequence 1, Application US/10283023  
Publication No. US2003091573A1  
GENERAL INFORMATION:  
APPLICANT: Carroli, Joseph M.  
TITLE OF INVENTION: Methods and compositions for the  
TITLE OF INVENTION: diagnosis and treatment of hematological disorders using  
FILE OF INVENTION: 16319  
FILE REFERENCE: MP101-2391RM  
CURRENT APPLICATION NUMBER: US/10/283,023  
CURRENT FILING DATE: 2002-10-29  
PRIOR APPLICATION NUMBER: 60/335,044  
PRIOR FILING DATE: 2001-10-31  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: FASTSEQ for Windows Version 4.0

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; SEQ ID NO 1
; LENGTH: 1705
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-283-023-1

Alignment Scores:
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Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x US-10-283-023-1 (1-1705)

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Db 226 GTAGAGCTTCGGCAGATTATCCCGTGTGAACCATCTTAATTTGTAAGCTTTATGAGACC 285
QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40
Db 286 TECTTGAATCCAGTGTGCTGTGATGGAATAATGCTGAAGGGGCTCTTATATTAATGTG 345
QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisSalMetSerTyrCysLeu 60
Db 346 CTGCATGTGCTGGAACCATTTGCATATTAATCTGCTGCCACGCAATGAGTGTGTTTA 405
QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProValAlaLeuIleHisArg 80
Db 406 CAGTGTCCCAAGGAGTGGCTTATCTTCACAGATGCAACCAAGCGCTAATTCACAGG 465
QY 81 AspLeuIleProAsnLeuLeuValAlaGlyGlyThrValIleuIleCysAsp 100
Db 466 GACCTGAAACCAACCAATTTACTGCTGTTCAAGGGGAGACAGTTCTTAAATAATTTGAT 525
QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnGlySerAlaAlaTyr 120
Db 526 TTGTGTACAGCTGTGATTCATTCACACACATGACCAATTAACAAGGGAGTGTGCTTGG 585
QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluIleCysAspValPheSerTyr 140
Db 586 ATGGCACCCTGAAGTTTGAAGGTAGTAATTAACAGTAATAAATGTGACGCTTCACCTGG 645
QY 141 GlyIleIleLeuTyrGluValIleThrArgArgIleProPheAspGluIleGlyIlePro 160
Db 646 GGTATATCTCTTGGGAAGTGAATACGCGGAAACCTTTGATGAGATGGTGCCCA 705
QY 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleIleAsnLeu 180
Db 706 GCTTTCGAAATCAATGAGGCTGTTCATTAATGTAATGTAACCACTGATTAATAAATTTA 765
QY 181 ProIleProIleGluSerLeuMetThrArgCysTyrSerIleAspProSerGlnArgPro 200
Db 766 CTTAAGCCCATTAAGAGCTGATGACTCGTTGTGTGTTAAGATCTTTCCAGGCGCTT 825
QY 201 SerMetGluGluIleValIleHisIleMetThrHisIleMetArgTyrPheProGlyAlaAsp 220
Db 826 TCAATGAGAGAAATTTGAAAATTAATGACTCACTTGATGCGGTACTTTCCAGAGACAGAT 885
QY 221 GluProLeuGlnTyrProCysGln 228
Db 886 GAGCCATTACAGATCTCTGTGAG 909

RESULT 2
US-10-283-023-3
; Sequence 3, Application US/10283023
; Publication No. US20030091573A1
; GENERAL INFORMATION:
; APPLICANT: Caroll, Joseph M.
; TITLE OF INVENTION: Methods and compositions for the
; TITLE OF INVENTION: diagnosis and treatment of hematological disorders using
; TITLE OF INVENTION: 16319
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FILE REFERENCE: MP101-239P1RM
; CURRENT APPLICATION NUMBER: US/10/283,023
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1705
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1557)
US-10-283-023-3

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Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x US-10-283-023-3 (1-1705)

QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIleLeuTyrGlyAla 20
Db 226 GTAGAGCTTCGGCAGATTATCCCGTGTGAACCATCTTAATTTGTAAGCTTTATGAGACC 285
QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40
Db 286 TECTTGAATCCAGTGTGCTGTGATGGAATAATGCTGAAGGGGCTCTTATATTAATGTG 345
QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisSalMetSerTyrCysLeu 60
Db 346 CTGCATGTGCTGGAACCATTTGCATATTAATCTGCTGCCACGCAATGAGTGTGTTTA 405
QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProValAlaLeuIleHisArg 80
Db 406 CAGTGTCCCAAGGAGTGGCTTATCTTCACAGATGCAACCAAGCGCTAATTCACAGG 465
QY 81 AspLeuIleProAsnLeuLeuValAlaGlyGlyThrValIleuIleCysAsp 100
Db 466 GACCTGAAACCAACCAATTTACTGCTGTTCAAGGGGAGACAGTTCTTAAATAATTTGAT 525
QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnGlySerAlaAlaTyr 120
Db 526 TTGTGTACAGCTGTGATTCATTCACACACATGACCAATTAACAAGGGAGTGTGCTTGG 585
QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluIleCysAspValPheSerTyr 140
Db 586 ATGGCACCCTGAAGTTTGAAGGTAGTAATTAACAGTAATAAATGTGACGCTTCACCTGG 645
QY 141 GlyIleIleLeuTyrGluValIleThrArgArgIleProPheAspGluIleGlyIlePro 160
Db 646 GGTATATCTCTTGGGAAGTGAATACGCGGAAACCTTTGATGAGATGGTGCCCA 705
QY 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleIleAsnLeu 180
Db 706 GCTTTCGAAATCAATGAGGCTGTTCATTAATGTAATGTAACCACTGATTAATAAATTTA 765
QY 181 ProIleProIleGluSerLeuMetThrArgCysTyrSerIleAspProSerGlnArgPro 200
Db 766 CTTAAGCCCATTAAGAGCTGATGACTCGTTGTGTGTTAAGATCTTTCCAGGCGCTT 825
QY 201 SerMetGluGluIleValIleHisIleMetThrHisIleMetArgTyrPheProGlyAlaAsp 220
Db 826 TCAATGAGAGAAATTTGAAAATTAATGACTCACTTGATGCGGTACTTTCCAGAGACAGAT 885
QY 221 GluProLeuGlnTyrProCysGln 228
Db 886 GAGCCATTACAGATCTCTGTGAG 909
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RESULT 3
US-10-386-414-12
; Sequence 12, Application US/10386414
; Publication No. US2004000616A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Robison, Keith E.
; APPLICANT: White, David
; APPLICANT: Williamson, Mark W.
; APPLICANT: Cook, William James
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
; FILE REFERENCE: ME103-0210NMIM
; CURRENT APPLICATION NUMBER: US/10/386,414
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/254,037
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/833,082
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1705
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-386-414-12

Alignment Scores:
Pred. No.: 2,94e-152 Length: 1705
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x US-10-386-414-12 (1-1705)
QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIleLeuTyrcIValA 20
DB 226 GTAGAGCTTGCGAGCTTATCCCGTGTGAACCACTCTTAATATTGTAACCTTTATGAGACC 285
QY 21 CysLeuAsnProValCysLeuValMetGluTyraIagIugIyGlySerLeuTyraAsnVal 40
DB 286 TGCCTGATTCAGAGTGTCTTGTATGATGATGCTGAAGGGGCTCTTTATATATATG 345
QY 41 LeuHisGlyValagIuProLeuProTyrtThraIaaIahIasIaMetSerThpCysLeu 60
DB 346 CTGACTGTGTGGAACCACTGCAATATTAATCTGCTGCCAGCAATGAGTGGGTGTTA 405
QY 61 GlnCysSerGlnGlyValAlaIaTyrlLeuHisSerMetGlnProIyValAlaLeuIleHisArg 80
DB 406 CAGTGTCCCAAGAGAGTGGCTTATCTTCACAGCATGCAACCAAGCGCTAATTCACAGG 465
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RESULT 4
US-10-158-895-14
; Sequence 14, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIIKO
; APPLICANT: TSUCHIYA, MASAUYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1776)
US-10-158-895-14

Alignment Scores:
Pred. No.: 3.14e-152 Length: 1788
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x US-10-158-895-14 (1-1788)
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DB 81 AspleuIySPProAsnLeuLeuValAlaGlyGlyThryValLeuIySileCysASP 100
DB 466 GACCTGAAACCAACCAACTTACTGCTGTCAGGGGGGAGACGTTCAAAAATTTGTGAT 525
QY 101 PheGIYThraIaCysaPillEGInThrhIsmetThraSnaIyGlySerAlaIaETP 120
DB 526 TTTGGTACAGCTGTGACATTTCAGACACATGACCAATTAACAAAGGAGGTGCTGTGG 585
QY 121 MetAlaProGluValIleGluGlySerArgTySercIuIySCysaSPValIleSerTTP 140
DB 586 ATGCACACCTTAAGTTTGAAGTAGTAATTAACGTAAAAAGTGAAGCTTGAGCTGG 645
QY 141 GlyIleIleLeuTyrcIValAlaIleThraArgArgIySPProPheAspGluIleGlyPro 160
DB 646 GGTATTATTCTTTGGGAAGAGATACCCGTCGAAACCTTTATAGATTGGTGGCCA 705
QY 161 AlaPheArgIleMetTTPAlaValIleAsnGlyThryArgProProLeuIleYAsnLeu 180
DB 706 GCTTCCGAATCAATGTGGGCTGTTCAATATGTACTGACCAACCATGATTAATAATTTA 765
QY 181 ProIySProlIegIuSerLeuMetThraGlycETPserIySASPProSerGlnArgPro 200
DB 766 CCTAAGCCCATGTGAACCTGATGATCATCGTGTGTCTAAAGATCCCTCCAGCGCCT 825
QY 201 SerMetGluIuIleValIySileMetThrhIsmetArgTyrcPheProGlyAlaASP 220
DB 826 TCAATGAGAGAAATGTGAATAATATATCATCTTAATGCGGTACTTCCAGAGCAT 885
QY 221 GluProLeuGlnTyrcProCysGln 228
DB 886 GAGCCATTACAGTATCCTTGTGCAG 909
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Db 232 GTAGAGCTTCGGAGTATCCCGCTGGAACCACTTAATATGTAAGCTTATGAGGCC 291
Qy 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40
Db 292 TGCTGAATCCAGTGTGCTTGTGATGAAATATGCTGAAGGGGGCTCTTATATATATG 351
Qy 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
Db 352 CTGACATGTCGTAACCATTCATATATATGCTGACCGCCACGCAATGATGGTGTTA 411
Qy 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProValAlaLeuHisArg 80
Db 412 CAGTGTTCCTCCAGAGAGTGCCTTATCTTCAACAGATGCAACCCAAAGCCTAATTCACAG 471
Qy 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
Db 472 GACCTGAAACCAACCAACTTACTGCTGGTTCAGGGGGGACGTTCTMAAATTTGTGAT 531
Qy 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnLeuLysGlySerAlaAlaTyr 120
Db 532 TTTGGTACAGCCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTGTGCTTGG 591
Qy 121 MetAlaProGluValPheGluGlySerAsnTyrSerGlnLysCysAspValPheSerTyr 140
Db 592 ATGGCACCCTGAAGTTTGAAGTAGTATTACAGTGAAATATGACGCTTCAAGCTCG 651
Qy 141 GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyPro 160
Db 652 GGTATTTATCTTTGGGAAAGTATTAACGGGTGGAACCCCTTGTAGATGGTGGCCCA 711
Qy 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
Db 712 GCTTCCGAATCATGTGGGCTGTTCAATATGTAATCTGACCAACCACTGATTAATAATTA 771
Qy 181 ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 200
Db 772 CCTAAGCCCATGTAAGAGCTGATGACTGCTGTGGCTTAAGATCCTTCCAGCCGCC 831
Qy 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
Db 832 TCATGAGAGGAATTTGGAAATATATGACTTGTATGCGGTACTTTCAGAGAGAGAT 891
Qy 221 GluProLeuGlnTyrProCysGln 228
Db 892 GAGCCATTACAGTATCCTGTGAG 915

RESULT 5
US-10-384-743-14
; Sequence 14, Application US/10384743
; Publication No. US20030162228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/384,743
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
```

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LOCATION: (7) .. (1786)
US-10-384-743-14

Alignment Scores:
Pred. No.: 3,14E-152
Score: 1252.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 16
Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x US-10-384-743-14 (1-1788)

Qy 1 ValGluLeuLeuGluLeuSerArgValAlaHisProAsnIleValLysLeuTyrGlyAla 20
Db 232 GTAGAGCTTCGGAGTATCCCGCTGGAACCACTTAATATGTAAGCTTATGAGGCC 291
Qy 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40
Db 292 TGCTGAATCCAGTGTGCTTGTGATGAAATATGCTGAAGGGGGCTCTTATATATATG 351
Qy 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
Db 352 CTGACATGTCGTAACCATTCATATATATGCTGACCGCCACGCAATGATGGTGTTA 411
Qy 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProValAlaLeuHisArg 80
Db 412 CAGTGTTCCTCCAGAGAGTGCCTTATCTTCAACAGATGCAACCCAAAGCCTAATTCACAG 471
Qy 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
Db 472 GACCTGAAACCAACCAACTTACTGCTGGTTCAGGGGGGACGTTCTMAAATTTGTGAT 531
Qy 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnLeuLysGlySerAlaAlaTyr 120
Db 532 TTTGGTACAGCCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTGTGCTTGG 591
Qy 121 MetAlaProGluValPheGluGlySerAsnTyrSerGlnLysCysAspValPheSerTyr 140
Db 592 ATGGCACCCTGAAGTTTGAAGTAGTATTACAGTGAAATATGACGCTTCAAGCTCG 651
Qy 141 GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyPro 160
Db 652 GGTATTTATCTTTGGGAAAGTATTAACGGGTGGAACCCCTTGTAGATGGTGGCCCA 711
Qy 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
Db 712 GCTTCCGAATCATGTGGGCTGTTCAATATGTAATCTGACCAACCACTGATTAATAATTA 771
Qy 181 ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 200
Db 772 CCTAAGCCCATGTAAGAGCTGATGACTGCTGTGGCTTAAGATCCTTCCAGCCGCC 831
Qy 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
Db 832 TCATGAGAGGAATTTGGAAATATATGACTTGTATGCGGTACTTTCAGAGAGAGAT 891
Qy 221 GluProLeuGlnTyrProCysGln 228
Db 892 GAGCCATTACAGTATCCTGTGAG 915

RESULT 6
US-10-158-895-3
; Sequence 3, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
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PRIOR APPLICATION NUMBER: US/09/529,279  
 PRIOR FILING DATE: 2000-04-11  
 PRIOR APPLICATION NUMBER: PCT/JP98/04796  
 PRIOR FILING DATE: 1998-10-22  
 PRIOR APPLICATION NUMBER: JP 9/290188  
 PRIOR FILING DATE: 1997-10-22  
 NUMBER OF SEQ ID NOS: 48  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 3  
 LENGTH: 2656  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (183)..(1919)  
 US-10-158-895-3

Alignment Scores:  
 Pred. No.: 5,44e-152 Length: 2656  
 Score: 1252.00 Matches: 228  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0

US-09-830-144-2\_COPY\_76\_303 (1-228) x US-10-158-895-3 (1-2656)

1 ValGluLeuAaGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyGlyAla 20  
 408 GTAGAGCTTCGGCAGGTATCCCGTGTGACCATCTAATATTGTAAGCTTATGAGACC 467  
 21 CysLeuAsnProValCysLeuValMetGluTyAlaGluGlyGlySerLeuTyAsnVal 40  
 468 TGCTTGAATCAGAGTGTCTTGATGATGAAATATGCTGAAAGGGGCTCTTTATATATG 527  
 41 LeuHisGlyAlaGluProLeuProTyTyThrAlaAlaHisAlaMetSerTrpCysLeu 60  
 528 CTGATGTGTGTGAACCATTCACATTAATTAATCTGCTGCCACGCAATGAGTGTGTTTA 587  
 61 GlnCysSerGlnGlyValAlaTyrlLeuHisSerMetGlnProLysAlaLeuIleHisArg 80  
 588 CAGGTTCCTCCAGAGTGTCTTATCTTCACAGCATGCAACCAAGCCTAATTCACAGG 647  
 81 AspleuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100  
 648 GACCTGAACACCAAACTTACTGCTGCTGCAAGGGGGAACAGTTCTAAATAATTTGTAT 707  
 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnLysGlySerAlaAlaTrp 120  
 708 TTTGTACAGCTGTGACATTCAGACACATGACCAATTAACAGGGAGTGTCTGTGG 767  
 121 MetAlaProGluValPheGluGlySerAsnTySerGluLysCysAspValPheSerTrp 140  
 768 ATGGACCTGAAGTTTGAAGGTATTAACGTGAAATGTAAGCTTCTACGCTGG 827  
 141 GlyIleIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyCysPro 160  
 828 GGTATTAATCTTTGGGAAGTAAACGGGTGCAACCTTTGATGAGATGCTGGCCCA 887  
 161 AlaPheArgIleMetTrpAlaValHisGlyThrArgProProLeuIleLysAsnLeu 180  
 888 GCTTCCCAATCATCTGGCTGTTCATATGCTACCAACCACTATTAATAAATTTA 947  
 181 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200  
 948 CTTAAGCCCATTTGAAGCTGATGCTGTTTGTCTTAAGATCTTCCAGGCGCT 1007  
 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyPheProGlyAlaAsp 220  
 1008 TCAATGAGGAAATTTGTGAATAATATGACTCACTTGAACGGTACTTTCAGAGACAGAT 1067  
 221 GluProLeuGlnTyTrpCysGln 228

Db 1068 GAGCCATTACAGTATCTTGTGAG 1091

RESULT 7

US-10-384-743-3  
 Sequence 3, Application US/10384743  
 Publication No. US2003016228A1  
 GENERAL INFORMATION:  
 APPLICANT: ONO, KOICHIRO  
 APPLICANT: OHTOMO, TOSHIHIRO  
 APPLICANT: TSUCHIYA, MASAYUKI  
 TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
 FILE REFERENCE: 053466/0278  
 CURRENT APPLICATION NUMBER: US/10/384,743  
 CURRENT FILING DATE: 2003-03-11  
 PRIOR APPLICATION NUMBER: US/09/529,279  
 PRIOR FILING DATE: 2000-04-11  
 PRIOR APPLICATION NUMBER: PCT/JP98/04796  
 PRIOR FILING DATE: 1998-10-22  
 PRIOR APPLICATION NUMBER: JP 9/290188  
 PRIOR FILING DATE: 1997-10-22  
 NUMBER OF SEQ ID NOS: 48  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 3  
 LENGTH: 2656  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (183)..(1919)  
 US-10-384-743-3

Alignment Scores:  
 Pred. No.: 5,44e-152 Length: 2656  
 Score: 1252.00 Matches: 228  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0

US-09-830-144-2\_COPY\_76\_303 (1-228) x US-10-384-743-3 (1-2656)

1 ValGluLeuAaGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyGlyAla 20  
 408 GTAGAGCTTCGGCAGGTATCCCGTGTGACCATCTAATATTGTAAGCTTATGAGACC 467  
 21 CysLeuAsnProValCysLeuValMetGluTyAlaGluGlyGlySerLeuTyAsnVal 40  
 468 TGCTTGAATCAGAGTGTCTTGATGATGAAATATGCTGAAAGGGGCTCTTTATATATG 527  
 41 LeuHisGlyAlaGluProLeuProTyTyThrAlaAlaHisAlaMetSerTrpCysLeu 60  
 528 CTGATGTGTGTGAACCATTCACATTAATTAATCTGCTGCCACGCAATGAGTGTGTTTA 587  
 61 GlnCysSerGlnGlyValAlaTyrlLeuHisSerMetGlnProLysAlaLeuIleHisArg 80  
 588 CAGGTTCCTCCAGAGTGTCTTATCTTCACAGCATGCAACCAAGCCTAATTCACAGG 647  
 81 AspleuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100  
 648 GACCTGAACACCAAACTTACTGCTGCTGCAAGGGGGAACAGTTCTAAATAATTTGTAT 707  
 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnLysGlySerAlaAlaTrp 120  
 708 TTTGTACAGCTGTGACATTCAGACACATGACCAATTAACAGGGAGTGTCTGTGG 767  
 121 MetAlaProGluValPheGluGlySerAsnTySerGluLysCysAspValPheSerTrp 140  
 768 ATGGACCTGAAGTTTGAAGGTATTAACGTGAAATGTAAGCTTCTACGCTGG 827  
 141 GlyIleIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyCysPro 160  
 828 GGTATTAATCTTTGGGAAGTAAACGGGTGCAACCTTTGATGAGATGCTGGCCCA 887

QY	161	AlaPheArgIleMetThrAlaValHisAsnGlyThrArgProProleuIleLysAsnLeu	180
Db	888	GCCTTCGATCATGAGGGGCTGTCTCAAAATGATCTGACCACTGATTTAAATAATTTA	947
QY	181	ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro	200
Db	948	CCTAACCCCATGAGAGCCCTGATGACTCGGTGTGTCAAAAGATCTTCCAGGCCCT	1007
QY	201	SerMetGluGlnIleValIleLysIleMetThrHisLeuMetArgTrpPheProGlyAlaAsp	220
Db	1008	TCAATGAGGAAATATGTGAAAATAAATGAAGCTCACTGATGCGTACTTTCAGAGACAGAT	1067
QY	221	GluProLeuGlnIleTrpProCysGln	228
Db	1068	GAGCCATTACAGATCTTGTGTGAG	1091
RESULT 8			
US-10-343-710-107			
/ Sequence 107, Application US/10343710			
/ Publication No. US20040087478A1			
/ GENERAL INFORMATION:			
/ APPLICANT: GILLEN, Clements			
/ APPLICANT: METZELS, Ingrid			
/ APPLICANT: MENDT, Stephan			
/ APPLICANT: WEIHE, E.			
/ APPLICANT: SCHAEFER, M., K.-H.			
/ TITLE OF INVENTION: SCREENING METHOD			
/ FILE REFERENCE: 029310.52022US			
/ CURRENT APPLICATION NUMBER: US/10/343,710			
/ CURRENT FILING DATE: 2003-09-17			
/ PRIOR APPLICATION NUMBER: PCT/EP01/09011			
/ PRIOR FILING DATE: 2001-08-03			
/ NUMBER OF SEQ ID NOS: 157			
/ SOFTWARE: PatentIn version 3.2			
/ SEQ ID NO 107			
/ LENGTH: 2769			
/ TYPE: DNA			
/ ORGANISM: Homo sapiens			
US-10-343-710-107			
Alignment Scores:			
Pred. No.: 5.76e-152 Length: 2769			
Score: 1252.00 Matches: 228			
Percent Similarity: 100.00% Conservative: 0			
Best Local Similarity: 100.00% Mismatches: 0			
Query Match: 100.00% Indels: 0			
DB: 18 Gaps: 0			
US-09-830-144-2_COPY_76_303 (1-228) x US-10-343-710-107 (1-2769)			
QY	1	ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIySLeuTyrgIyAla	20
Db	388	GTAAGAGCTTGCGGACGATTATCCCGTGTCAGACCATCTTAATGTGTAAGCTTTATGAGGCC	447
QY	21	CysLeuAsnProValCysLeuValMetGlnTyralGlnIlyGlySerLeuTyraSnVal	40
Db	448	TGCTTGAATCAAGTGTCCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATTAATATGG	507
QY	41	LeuHisGlyAlaGluProLeuProTyTrpThrAlaAlaHisAlaMetSerTrpCysLeu	60
Db	508	CTGCATGTGCTGTAACCATTTGACATATTATACGTGTCGCCACGCAATGAGTTGTGTTTA	567
QY	61	GlnCysSerGlnGlyValAlaTyTrpLeuHisSerMetGlnProLysAlaLeuIleHisArg	80
Db	568	CAGTGTCCCAAGAGAGTGCGTTATCTTCACAGCATGCMAACCCAAAGCGCTAATTCCAGG	627
QY	81	AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp	100
Db	628	GACCTGAACCAACAACTTACTGCTGTGGTTGCGAGGGGGGACAGCTTTAATAATTTGTGAT	687
QY	101	PheGlyThrAlaLysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp	120
Db	688	TTTGTGACGCGGTGATCAATTCAACAACATACCAATTAACAAGGGAGTCTGCTTGG	747

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QY      121  MetAlProGluValPheGluGlySerAluYrSerGluGlySerAluPheSerTrp 140
Db      748  ATGGACCTGAAGTTTGAAGTACTAATTCACGAGAAAATGACGCTTCACCTGG 807

QY      141  GlyTlleIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 160
Db      808  GGATTAATTCCTTGGAGAGTGATTAACGCGCTCGGAAACCTTTGATGATGATGGTGGCCCA 867

QY      161  AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProleuIleLysAsnLeu 180
Db      868  GCCTTCCGATCATGTGGGCTGTTCAATATGTACTCGACCACTGATATAAAAATTTA 927

QY      181  ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGluArgPro 200
Db      928  CCTAAGCCCATGAGAGCGCTGATGACTCGTGTGGTCTAAAGATTCCTTCCAGGGCCCT 987

QY      201  SerMetGluGluIleValLysIleMetThrHisLeuMetArgTrpPheProGlyAlaAsp 220
Db      988  TCATATCGAGAGAAATGTGAAATTAATGACTCATCTTAATCGGATCTTTCAGAGACAGAT 1047

QY      221  GluProLeuGluInTyProCysGln 228
Db      1048  GAGCCATTACAGTATCTGTGCAG 1071

RESULT 9
US-10-263-929-85
; Sequence 85, Application US/10263929
; Publication No. US20040067535A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Alzheimer's Disease Linked Genes
; FILE REFERENCE: LSD-07417
; CURRENT FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: Version 3.2
; SEQ ID NO 85
; LENGTH: 2865
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-263-929-85

Alignment Scores:
Pred. No.:      6,77e-40      Length:      2865
Score:          392.50      Matches:      88
Percent Similarity: 56.68%      Conservative: 35
Best local Similarity: 40.55%      Mismatches:  77
Query Match:     31.35%      Indels:      17
Db:              18          Gaps:          6

US-09-830-144-2_COPY_76_303 (1-228) x US-10-263-929-85 (1-2865)
QY      2      GluLeuArgGluLeuSerArgValAlaAsnHisProAsnIleValLysLeuTyArgAlaCys 21
Db      433  GAAGCCCGGCTCTTTGGAGCCCTGCGACACCCCAACATAATATGCCCTTAAGGGGCGCTGC 492

QY      22  LeuAsnPro-----ValCysLeuValMetGlyTrpAlaGluGlyGlySerLeuTyArgSn 39
Db      493  CTAAACCCCCACACACCTCTGCTAGATGATGAGTATAGCCCGGAGTGGTGACAGAGAGG 552

QY      40  ValLeuHisGlyAlaGluProLeuProTyTrpThrAlaAlaHisAlaMetSerTrpCys 59
Db      553  GTCTGCGAGGTGGCCGGGCTGACCTCACTG------CTGTCACACTGGGCT 600

QY      60  LeuGlnCysSerGlnGlyValAlaLysIleSerMetGlnProLysAlaLeuIleHis 79
Db      601  GTCCAGATGTGCGCGGGGCAATGAATCACTAACACAATGATAGCCCTGTGCCATCATCCAC 660

QY      80  ArgAspLeuLysProProleuLeuLeuVal-----AlaGly 92
Db      661  CGGGAACCTTAATGCATCAACATCCGTGATCCGTGAGCGATGAGGCAATGAGAACCAACACTTGGCA 720

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RESULT 9
US-10-263-929-85
; Sequence 85, Application US/10263929
; Publication No. US20040067535A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Alzheimer's Disease Linked Genes
; FILE REFERENCE: LSD-07417
; CURRENT APPLICATION NUMBER: US/10/263,929
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
; LENGTH: 2865
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-263-929-85

Alignment Scores:
Pred. NO.:          6,77e-40          Length:          2865
Score:              392.50            Matches:          88
Percent Similarity: 56.68%            Conservative:     35
Best Local Similarity: 40.55%          Mismatches:      77
Query Match:        31.35%            Indels:          17
DB:                  18                Gaps:            6

US-09-830-144-2_COPY_76_303 (1-228) x US-10-263-929-85 (1-2865)
QY      2  G|U|U|U|A|G|G|U|U|U|U|U|U|S|E|T|A|G|V|A|A|S|N|H|I|A|P|R|O|A|S|N|I|U|E|V|A|L|U|S|Y|S|E|U|Y|G|I|A|A|C|Y|S 21
Db      433 GAAAGCCCGGCGCTCTTTTGAGAGCCCTTGACAGCACCACCAACATATATGTCCTTTAGGGGGCGCTCG 432
QY      22  L|E|A|S|N|P|R|O|-----|V|A|L|Y|S|E|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U| 39
Db      493 CTGACACCCGCCACACACCTCTGCTCCCTAGAGATGAGATGAGCCCGGGGTGGTGACCTGACGAG 552
QY      40  V|A|L|U|U|H|I|S|G|I|Y|A|L|A|G|U|P|R|O|L|E|U|P|P|R|O|Y|T|Y|T|H|R|A|L|A|H|I|S|A|L|U|E|S|E|T|P|C|Y|S 59
Db      553 GTGCTGGACAGGTGGCCGGGGTGCACCTTACAGT------CTGGTCAACTGGGCT 600
QY      60  L|E|U|G|I|N|C|Y|S|E|R|G|I|N|G|I|Y|A|L|A|T|Y|L|U|U|H|I|S|E|S|E|T|E|C|I|N|P|R|O|L|Y|S|A|L|U|U|I|U|H|S 79
Db      601 GTGCAAGTGGCCCGGGGGGCATGAACTACTTACACAAATGATGCCCTGTGCCCATTCAC 660
QY      80  A|T|G|A|S|P|L|U|U|Y|P|R|O|A|S|N|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U|U| 92
Db      661 CGGGAAGCTCAAGTTCATCAACATCCCTGATCTCTGAGCTGGAGGCCATGAGAACCAACCACTTGCA 720

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Oy 31yhrVAlleuVylleCyAspPhegIyThraIaCyAsp---IlEgIThHsmet 111
Db 721 GACCGGCTGCATMAATACGAGACTTGCGCTCGCCCGCGAGTGCACAAAGCACCAAG 780
Oy 112 ThraAnEnuVgIySerAlAlaTrpMetAlaProGluValPheGluGlySerAnTyr 131
Db 781 ATGAGCGGTGGGGGAGACTAGCGCTGAGTGGGCGGAGGTATACGCTCTCCTCTTC 840
Oy 132 SerGluTyrCyAspValPheSerTrpGlyIleIleuTrpGluValIleThrArgArg 151
Db 841 TCCAAACACAGTGAATGCTCGAGCTCGGGGCTGCTGGGAGACTGCTGACGGGGAG 900
Oy 152 LysProPheAspGluIleGlyGlyProAlaPheArgIleMetTrpAlaVal---HisAsn 170
Db 901 GTCCCTTACCGTGAATC-----GACGCTTGGCCGTGGCGCTAAGCGCTGCTGAAT 954
Oy 171 GlyThrArgProProIleuIleLysAsnLeuProIleGluSerIleuMetThrArg 190
Db 955 AAGCGAGAGTGGCCCATTCCTCCACGTGGCCCGAGCCCTTGCCCGCTCCTGAGGAA 1014
Oy 191 CyTrpSerLysAspProSerGlnArgProSerMetGluGluIleValIys 207
Db 1015 TGCTGGAGCCGACAGACCCCAACGGGCGGCGCAATTCGTAGACATCTTGAAG 1065

RESULT 10
US-10-369-022-55
/ Sequence 55, Application US/10369022
/ Publication No. US20030203847A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: Rosenfeld, Julie Beth
/ APPLICANT: Siles-Santiago, Immaculada
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
/ TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
/ TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 316, 636,
/ TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
/ TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
/ TITLE OF INVENTION: 13424 MOLECULES
/ FILE REFERENCE: MP102-027P1R0M0T1M
/ CURRENT APPLICATION NUMBER: US/10/369,022
/ CURRENT FILING DATE: 2003-02-19
/ PRIOR APPLICATION NUMBER: US 60/360,495
/ PRIOR FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: US 60/370,121
/ PRIOR FILING DATE: 2002-04-04
/ PRIOR APPLICATION NUMBER: US 60/373,010
/ PRIOR FILING DATE: 2002-04-16
/ PRIOR APPLICATION NUMBER: US 60/373,908
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: US 60/377,717
/ PRIOR FILING DATE: 2002-05-03
/ PRIOR APPLICATION NUMBER: US 60/379,949
/ PRIOR FILING DATE: 2002-05-13
/ PRIOR APPLICATION NUMBER: US 60/382,409
/ PRIOR FILING DATE: 2002-05-21
/ PRIOR APPLICATION NUMBER: US 60/385,280
/ PRIOR FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: US 60/386,879
/ PRIOR FILING DATE: 2002-06-06
/ PRIOR APPLICATION NUMBER: US 60/387,536
/ PRIOR FILING DATE: 2002-06-10
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 55
/ LENGTH: 3138
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (161)...(3022)
/ US-10-369-022-55

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Alignment Scores:	7.68e-40	Length:	3138
Pred. No.:	392.50	Matches:	88
Score:	56.68%	Conservative:	35
Percent Similarity:	40.55%	Mismatches:	77
Best Local Similarity:	31.35%	Indels:	17
Query Match:	17	Gaps:	6

US-09-830-144-2\_COPY\_76\_303 (1-228) x US-10-369-022-55 (1-3138)

QY	2	GLULEuArgrLnLeuSerArVAlAsnHiPrOAsnHLeValVysLeuTyrGlyAlaCys	21
Db	593	GAAGCCCGCTCTTGTGAGCCCTCGACAGACCCCAACAAATATGCTTTAGGGGCGCTGC	652
QY	22	LeuAsnPro-----ValCysLeuValMetGlnTyrAlaGlnGlyGlySerLeuTyrAsn	39
Db	653	CTCAACCCCCACACACTCTGCTCTAGTAGAGTAGATGCCCGGGGTGGTGACACTAGACAG	712
QY	40	ValLeuHIsGlyAlaGlnProLeuProTyrTyrThraAlaAlaHIsAlaMetSerTyrCys	59
Db	713	GGCTGGAGAGGTCGGCGGCTGCACCTCACGTG-----CTGGTCAACTGGGCT	760
QY	60	LeuGlnCysSerGlnGlyValAlaTyrLeuHIsSerMetGlnProVysAlaLeuHIs	79
Db	761	GTGCGAGGTGGCCCGGGGGCATGAACTACTACATGATGATGCCCTGTGCCATCATTCAC	820
QY	80	ArgAspLeuLysProProAsnLeuLeuLeuVal-----AlaGly	92
Db	821	CGGAGCTCTCAAGTCCATCATCAACTCTTATCTCTGAGAGGCATCGAAGACCAACTCGCA	880
QY	93	GlyThrValLeuLysLeCysAspPheGlyThraAlaCysAsp--LleGlnThrHIsMet	111
Db	881	GACAGCGGTCTCAAGATCATCGGACTTTCGGCTTCGGCCCGGAGTGGCACAAGACCAAG	940
QY	112	ThraAsnAsnLysGlySerAlaAlaTyrMetAlaProGlnValPheGlnGlySerAsnTyr	131
Db	941	ATGACCGCTGCGGGGACCTTACGCCCTGATGGCGGAGGTTATCCGTCTCTCCCTTC	1000
QY	132	SerGlnLysCysAspValPheSerTyrGlyLeuLeuTyrGlnValIleThraArg	151
Db	1001	TCCAAAAGCATGATGTCTGAGACTTCGGGGTCTGCTGTGGAGCTCTGACGGGGAG	1060
QY	152	LysProPheAspGlnIleGlyGlyProAlaPheArgIleMetTyrAlaVal--HisAsn	170
Db	1061	GGCCCTTACCGGAGATC-----GACGCTTGGCGGTGAGCTATGGCTATGAT	1110
QY	171	GlyThrArgProProLeuIleLysAsnLeuProLysProIleGlnSerLeuMetThrArg	190
Db	1115	AAGCTGACGCTCCCATTCCTCCACAGTGCACCGCCGCTTGTCCCGCTCTCGAGGAA	1170
QY	191	CysTyrSerLysAspProSerGlnArgProSerMetGlnIleValLys	207
Db	1175	TGCTGGAGACCAAGACCCCAAGGGGGCCAGATTTCGTAGATCTTGAAG	1225

RESULT 11

US-10-210-120-86

Sequence 86, Application US/10210120

Publication No. US20030175736A1

GENERAL INFORMATION:

APPLICANT: Chinnaiyan, Arul M.

APPLICANT: Rubin, Mark A.

APPLICANT: Sreekumar, Arun

TITLE OF INVENTION: Expression Profile of Prostate Cancer

FILE REFERENCE: UM-07221

CURRENT APPLICATION NUMBER: US/10/210,120

CURRENT FILING DATE: 2002-08-01

PRIOR APPLICATION NUMBER: US 60/309,581

PRIOR FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: US 60/334,468

PRIOR FILING DATE: 2001-11-15

NUMBER OF SEQ ID NOS: 123

SOFTWARE: PatentIn version 3.2



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; SEQ ID NO 86
; LENGTH: 3435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-86

Alignment Scores:
Pred. No.:      8 71e-40      Length:      3435
Score:          392.50      Matches:      88
Percent Similarity: 56.68%      Conservative: 35
Best Local Similarity: 40.55%      Mismatches: 77
Query Match:     31.35%      Indels:     17
DB:              16      Gaps:           6

US-09-830-144-2_COPY_76_303 (1-228) x US-10-210-120-86 (1-3435)

QY      2  GtLeuArGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAlaCys 21
      Db  721 GAAGCCCGGCTCTTTGGAGCCCTTGACAGACCCCAACATATATGCCCCTTAGGGGCGCTGC 780
QY      22  LeuAsnPro-----ValCysLeuValMetGlnTyrAlaGlnGlyGlySerLeuTyrAsn 39
      Db  781 CTCAACCCCCCAACACCTCTGCTAGTATGAGTATGCCGGGGTGGTGCATGACAGAG 840
QY      40  ValLeuHisGlyAlaGlnProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCys 59
      Db  841 GTGCTGGACAGGTCCCGGGGTGCCACCTCACGTG-----CTGCTCACTGGGCT 888
QY      60  LeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHis 79
      Db  889 GTGACAGTGGCCCGGGGCGATGACACTTACCAATATATAGCCCTGTGCCCATATCTCAC 948
QY      80  ArgAspLeuLysProProAsnLeuLeuVal-----AlaGly 92
      Db  949 CGGAGCTTCAGATCCATCAACATCTGATCTGTAGAGGCCATCGAAGAACACCAACCTGCA 1008
QY      93  GlyThrValLeuLysIleCysAspPheGlyThrAlaCysAsp---IleGlnThrHisMet 111
      Db  1009 GACACGGTCTCCAGATACAGACTTGGGCTCGCCCGGACGTGGCAACAGACCCACAG 1068
QY      112  ThrAsnAsnLysGlySerAlaAlaTyrMetAlaProGlnValPheGlnGlySerAsnTyr 131
      Db  1069 ATGAGCCCTGCGGGGACCTACGCTGATGGCGCGAGGTATCCCTCTCTCCCTCTTC 1128
QY      132  SerGlnLysCysAspValPheSerTyrGlyIleLeuTyrGlnValIleThrArgArg 151
      Db  1129 TCCAAAGCACTGATGTCTGAGCTTGGGGTCTGCTGTGGAGCTGCTGACGCGGGAG 1188
QY      152  LysProPheAspGlnIleGlyGlyProAlaPheArgIleMetTyrAlaVal---HisAsn 170
      Db  1189 GTCCCTTACCGTAGATC-----GACGCTTGGCCGTGCGCGTATGGCGTGTATGAAT 1242
QY      171  GlyThrArgProProLeuIleLysAsnLeuProLysProIleGlnSerLeuMetThrArg 190
      Db  1243 AAGCTGACGCTGCCCATTTCCCTCACGTCGCCGAGACCCCTTTCGCCGCTCTCGAGGAA 1302
QY      191  CysTyrSerLysAspProSerGlnArgProSerMetGlnIleValLys 207
      Db  1303 TGCTGGAGCCAGACCCCAACGCGGCGGCGAGATTTGCTGATGACATCTTGAAG 1353

RESULT 12
US-10-909-035-86
; Sequence 86, Application US/10909035
; Publication No. US20050136493A1
; GENERAL INFORMATION:
; APPLICANT: Rubin, Mark A.
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Laxman, Bharathi
; APPLICANT: Sreekanth, Arun
; TITLE OF INVENTION: AMACR Cancer Markers
; FILE REFERENCE: UM-09098
; CURRENT APPLICATION NUMBER: US/10/909,035
; CURRENT FILING DATE: 2004-07-30

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; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
; LENGTH: 3435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-909-035-86

Alignment Scores:
Pred. No.:      8 71e-40      Length:      3435
Score:          392.50      Matches:      88
Percent Similarity: 56.68%      Conservative: 35
Best Local Similarity: 40.55%      Mismatches: 77
Query Match:     31.35%      Indels:     17
DB:              22      Gaps:           6

US-09-830-144-2_COPY_76_303 (1-228) x US-10-909-035-86 (1-3435)

QY      2  GtLeuArGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAlaCys 21
      Db  721 GAAGCCCGGCTCTTTGGAGCCCTTGACAGACCCCAACATATATGCCCCTTAGGGGCGCTGC 780
QY      22  LeuAsnPro-----ValCysLeuValMetGlnTyrAlaGlnGlyGlySerLeuTyrAsn 39
      Db  781 CTCAACCCCCCAACACCTCTGCTAGTATGAGTATGCCGGGGTGGTGCATGACAGAG 840
QY      40  ValLeuHisGlyAlaGlnProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCys 59
      Db  841 GTGCTGGACAGGTCCCGGGGTGCCACCTCACGTG-----CTGCTCACTGGGCT 888
QY      60  LeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHis 79
      Db  889 GTGACAGTGGCCCGGGGCGATGACACTTACCAATATATAGCCCTGTGCCCATATCTCAC 948
QY      80  ArgAspLeuLysProProAsnLeuLeuVal-----AlaGly 92
      Db  949 CGGAGCTTCAGATCCATCAACATCTGATCTGTAGAGGCCATCGAAGAACACCAACCTGCA 1008
QY      93  GlyThrValLeuLysIleCysAspPheGlyThrAlaCysAsp---IleGlnThrHisMet 111
      Db  1009 GACACGGTCTCCAGATACAGACTTGGGCTCGCCCGGACGTGGCAACAGACCCACAG 1068
QY      112  ThrAsnAsnLysGlySerAlaAlaTyrMetAlaProGlnValPheGlnGlySerAsnTyr 131
      Db  1069 ATGAGCCCTGCGGGGACCTACGCTGATGGCGCGAGGTATCCCTCTCTCCCTCTTC 1128
QY      132  SerGlnLysCysAspValPheSerTyrGlyIleLeuTyrGlnValIleThrArgArg 151
      Db  1129 TCCAAAGCACTGATGTCTGAGCTTGGGGTCTGCTGTGGAGCTGCTGACGCGGGAG 1188
QY      152  LysProPheAspGlnIleGlyGlyProAlaPheArgIleMetTyrAlaVal---HisAsn 170
      Db  1189 GTCCCTTACCGTAGATC-----GACGCTTGGCCGTGCGCGTATGGCGTGTATGAAT 1242
QY      171  GlyThrArgProProLeuIleLysAsnLeuProLysProIleGlnSerLeuMetThrArg 190
      Db  1243 AAGCTGACGCTGCCCATTTCCCTCACGTCGCCGAGACCCCTTTCGCCGCTCTCGAGGAA 1302
QY      191  CysTyrSerLysAspProSerGlnArgProSerMetGlnIleValLys 207
      Db  1303 TGCTGGAGCCAGACCCCAACGCGGCGGCGAGATTTGCTGATGACATCTTGAAG 1353

RESULT 13
US-09-969-347-226
; Sequence 226, Application US/09969347
; Patent No. US20020115085A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Cancer Gene Determination and Therapeutic Screening Using Signati
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-69
; CURRENT APPLICATION NUMBER: US/09/969,347
; CURRENT FILING DATE: 2001-10-02

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1 Sequence 8355, Application US/10843641A
2 Publication No. US20050064454A1
3
4 GENERAL INFORMATION:
5 APPLICANT: Avalon Pharmaceuticals, Inc.
6 TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
7 FILE OF INVENTION: Signature Gene Sets
8 FILE REFERENCE: 689290-189
9 CURRENT APPLICATION NUMBER: US/10/843,641A
10 CURRENT FILING DATE: 2004-05-12
11 PRIORITY APPLICATION NUMBER: US/09/873,367
12 PRIORITY FILING DATE: 2001-06-05
13 PRIORITY APPLICATION NUMBER: US/09/954,551
14 PRIORITY FILING DATE: 2001-09-18
15 PRIORITY APPLICATION NUMBER: US/09/954,456
16 PRIORITY FILING DATE: 2001-09-25
17 PRIORITY APPLICATION NUMBER: US/09/962,436
18 PRIORITY FILING DATE: 2001-09-25
19 PRIORITY APPLICATION NUMBER: US/09/962,832
20 PRIORITY FILING DATE: 2001-09-25
21 PRIORITY APPLICATION NUMBER: US/09/964,824
22 PRIORITY FILING DATE: 2001-09-27
23 PRIORITY APPLICATION NUMBER: US/09/967,768
24 PRIORITY FILING DATE: 2001-09-28
25 PRIORITY APPLICATION NUMBER: US/09/968,007
26 PRIORITY FILING DATE: 2001-10-02
27 PRIORITY APPLICATION NUMBER: US/09/969,347
28 PRIORITY FILING DATE: 2001-10-02
29 PRIORITY APPLICATION NUMBER: US/09/969,708
30 PRIORITY FILING DATE: 2001-10-03
31 Remaining Prior Application data removed - See File Wrapper or PALM.
32 NUMBER OF SEQ ID NOS: 8447
33 SOFTWARE: PatentIn version 3.0
34 SEQ ID NO 8355
35 LENGTH: 3454
36 TYPE: DNA
37 ORGANISM: Homo sapiens
38 US-10-843-641A-8355

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Alignment Scores:	
Pred. No.:	8,786-40
Score:	392.50
Percent Similarity:	56.68
Best Local Similarity:	40.55
Query Match:	31.35
DB:	21
Length:	3454
Matches:	86
Conservative:	35
Mismatches:	77
Indels:	17
Gaps:	6

US-09-830-144-2\_COPY\_76\_303 (1-228) x US-10-843-641A-8355 (1-3454)

QY 2 GNLLeuAlaG1LeuSerzrValAlaAmiSPProAniLeValLysLeuYrG1ValaCys 21  
Db 721 GAAGCCGGGCTCTTGGAGCCCTGGAGACACCCCAACATATATTCGCCCTTAAAGGGGGGCTGC 780  
QY 22 LeuAenPro-----ValCysLeuValaMetG1urYrAlaG1uG1ySerLeuYrAen 39  
Db 781 CTCACACCCCAACACCTCTGCTTATGATGGAGATATGCCGGGGTGGTGGATGGAGAG 840  
QY 40 ValLeuHisG1YrAlaG1uProLeuProYrYrThrAlaAlaHisAlaMetSerTrpCys 59  
Db 841 GTGCTGGACAGTGGCCGGGTGCCACTGACGTG-----CTGTCAACTGGGCT 888  
QY 60 LeuG1nCysSerG1uYrValAlaTrpLeuHisSerMetG1nProYrValaLeuLeHis 79  
Db 889 GTGCAGAGTGGCCCGGGGCAATGAATCACTTAACACATATATGCCCTGTGCCCACTTCCAC 948  
QY 80 ArgAerLeuYrProProAniLeuLeuVal-----AlaG1y 92  
Db 949 CGGAGCTCAAGTCATGACATCATCTGTATCTCTGGAGGCACTCCAGAACCAACACTTGGCA 1000  
QY 93 G1YrThrValLeuYrIleCysAspRheG1YrThrAlaCysAsp--IleG1nThrHisMet 111  
Db 1009 GACAGCGGTCTCAAGATCAACGAACTTGGCTCGCCCGGAGTGGGACAAAGACCAACAG 1066  
QY 112 ThrAenLeuYrG1ySerAlaAlaTrpMetAlaProG1uValPheG1uG1ySerAnYr 131

[illegible]

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Search completed: August 2, 2005, 23:16:46
Job time : 856.757 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: August 2, 2005, 17:23:41 ; Search time 55.8243 Seconds  
(without alignments)  
5979.480 Million cell updates/sec

Title: US-09-830-144-3\_COPY\_1338\_1541

Perfect score: 204  
Sequence: 1 caaagccgcagccttaacct.....agagcgtggtgacacacgcg 204

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PTCUS.COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	204	100.0	1560	2	US-08-752-891-1
2	204	100.0	1560	2	US-08-752-891-5
3	204	100.0	1560	2	US-09-144-178-1
4	204	100.0	1560	2	US-09-144-178-5
5	204	100.0	1560	3	US-09-406-854-1
6	204	100.0	1560	3	US-09-406-854-5
7	204	100.0	1560	3	US-09-529-279-1
8	204	100.0	1560	3	US-10-158-895-1
9	204	100.0	1568	3	US-09-529-279-42
10	204	100.0	1568	3	US-10-158-895-42
11	204	100.0	1569	3	US-09-529-279-10
12	204	100.0	1569	4	US-10-158-895-10
13	37.2	18.2	1278	4	US-09-252-991A-8932
14	37.2	18.2	1491	2	US-08-941-6647A-4
15	37.2	18.2	1505	3	US-09-142-481-1
16	37.2	18.2	1878	4	US-09-252-991A-9933
17	37.2	18.2	2211	4	US-09-252-991A-1927
18	36.4	17.8	591	4	US-10-101-464A-289
19	36.4	17.8	2380	4	US-10-101-464A-864
20	35.4	17.4	762	4	US-09-252-991A-3481
21	35.4	17.4	1203	4	US-09-252-991A-3468
22	35.4	17.4	1269	4	US-09-252-991A-3470
23	35.4	17.4	45314	4	US-09-949-016-14927
24	35.4	17.4	13424	4	US-09-949-016-13594
25	34	16.7	588	4	US-09-724-797-45
26	34	16.7	1896	4	US-08-426-630-33
27	34	16.7	4748	4	US-08-426-630-29

C 28	33.8	16.6	47981	4	US-09-679-279-1	Sequence 1, Appli
C 29	33.6	16.5	81001	3	US-09-750-580-1	Sequence 1, Appli
C 30	32.8	16.1	858	4	US-09-902-540-3668	Sequence 3668, Ap
C 31	32.8	16.1	1643	4	US-09-902-540-6808	Sequence 6808, Ap
C 32	32.8	16.1	4282	4	US-09-902-540-563	Sequence 563, App
C 33	32.8	16.1	23847	4	US-09-902-540-1177	Sequence 1177, Ap
C 34	32	15.7	807	4	US-09-902-540-6012	Sequence 6012, Ap
C 35	32	15.7	809	4	US-09-902-540-23	Sequence 1667, A
C 36	31.8	15.6	57978	4	US-09-949-016-16667	Sequence 16667, A
C 37	31.6	15.5	1206	4	US-09-902-540-4100	Sequence 4100, Ap
C 38	31.6	15.5	23738	4	US-09-902-540-1203	Sequence 1203, Ap
C 39	31.4	15.4	592	4	US-09-270-767-2308	Sequence 2308, Ap
C 40	31.4	15.4	592	4	US-09-270-767-17590	Sequence 17590, A
C 41	31.4	15.4	1980	4	US-09-902-540-9228	Sequence 9228, Ap
C 42	31.4	15.4	2007	4	US-09-976-594-407	Sequence 407, App
C 43	31.4	15.4	13234	4	US-09-902-540-986	Sequence 986, App
C 44	31.2	15.3	601	4	US-09-949-016-91879	Sequence 91879, A
C 45	31.2	15.3	601	4	US-09-949-016-194820	Sequence 194820,

## ALIGNMENTS

RESULT 1  
US-08-752-891-1  
Sequence 1, Application US/08752891  
Patent No. 5837819  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
APPLICANT: NISHIDA, Eisuke  
TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURES:  
NAME/KEY: CDS  
LOCATION: 30..1541  
FEATURE:  
NAME/KEY: mat\_peptide



NAME/KEY: CDS  
LOCATION: 30..1541  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 30..1541  
US-09-144-178-1

Query Match 100.0%; Score 204; DB 2; Length 1560;  
Best Local Similarity 100.0%; Pred. No. 3e-48;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 60  
DB 1338 CAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 1397  
QY 61 TCTGACGAGGCGCTCTTCGCTCCCGGCGCCGACCTGCTCCGCTGCGGAGACGGT 120  
DB 1398 TCTGACGAGGCGCTCTTCGCTCCCGGCGCCGACCTGCTCCGCTGCGGAGACGGT 1457  
QY 121 CGTGTGAGCCCTATGTGAGACTTTGCTGATTTTACCGCCCTGTGAGCGTGAACCAATGCG 180  
DB 1458 CGTGTGAGCCCTATGTGAGACTTTGCTGATTTTACCGCCCTGTGAGCGTGAACCAATGCG 1517  
QY 181 GAGCAGAGCGTGTGACGACGACCG 204  
DB 1518 GAGCAGAGCGTGTGACGACGACCG 1541

## RESULT 4

US-09-144-178-5  
Sequence 5, Application US/09144178

Patent No. 5989862

GENERAL INFORMATION:

APPLICANT: MATSUMOTO, Kunihiko

APPLICANT: NISHIDA, Eisuke

TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/144.178

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/752,891

FILING DATE: 20-NOV-1996

APPLICATION NUMBER: JP 8-300856

FILING DATE: 28-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 8-126282

FILING DATE: 24-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 17981/111

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1560 base pairs

TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 30..1541

FEATURE:

NAME/KEY: mat\_peptide

LOCATION: 30..1541

US-09-144-178-5

Query Match 100.0%; Score 204; DB 2; Length 1560;  
Best Local Similarity 100.0%; Pred. No. 3e-48;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 60  
DB 1338 CAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 1397  
QY 61 TCTGACGAGGCGCTCTTCGCTCCCGGCGCCGACCTGCTCCGCTGCGGAGACGGT 120  
DB 1398 TCTGACGAGGCGCTCTTCGCTCCCGGCGCCGACCTGCTCCGCTGCGGAGACGGT 1457  
QY 121 CGTGTGAGCCCTATGTGAGACTTTGCTGATTTTACCGCCCTGTGAGCGTGAACCAATGCG 180  
DB 1458 CGTGTGAGCCCTATGTGAGACTTTGCTGATTTTACCGCCCTGTGAGCGTGAACCAATGCG 1517  
QY 181 GAGCAGAGCGTGTGACGACGACCG 204  
DB 1518 GAGCAGAGCGTGTGACGACGACCG 1541

## RESULT 5

US-09-406-854-1

Sequence 1, Application US/09406854

Patent No. 6140042

GENERAL INFORMATION:

APPLICANT: MATSUMOTO, Kunihiko

APPLICANT: NISHIDA, Eisuke

TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/406.854

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/752,891

FILING DATE: 20-NOV-1996

APPLICATION NUMBER: JP 8-300856

FILING DATE: 28-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 8-126282

FILING DATE: 24-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 17981/111

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1541  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 30..1541  
US-09-406-854-1

Query Match 100.0%; Score 204; DB 3; Length 1560;  
Best Local Similarity 100.0%; Pred. No. 3e-48;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 60  
DB 1338 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 1397  
QY 61 TCTGACGAGGCGCTTTCCTCCGCTCCGCGCCGACCTGCTCCGCTGCGGAGACGCT 120  
DB 1398 TCTGACGAGGCGCTTTCCTCCGCTCCGCGCCGACCTGCTCCGCTGCGGAGACGCT 1457  
QY 121 CGTGTGAGCCCTTATGTGACCTTTGCTGATTTTACCGCCCTGAGAGCGTGAACATGCG 180  
DB 1458 CGTGTGAGCCCTTATGTGACCTTTGCTGATTTTACCGCCCTGAGAGCGTGAACATGCG 1517  
QY 181 GAGCAGAGCGTGTGACAGCACCG 204  
DB 1518 GAGCAGAGCGTGTGACAGCACCG 1541

## RESULT 6

US-09-406-854-5  
Sequence 5, Application US/09406854  
Patent No. 6140042  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
APPLICANT: NISHIDA, Ritsuke  
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BERT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1541  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 30..1541  
US-09-406-854-5

Query Match 100.0%; Score 204; DB 3; Length 1560;  
Best Local Similarity 100.0%; Pred. No. 3e-48;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 60  
DB 1338 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 1397  
QY 61 TCTGACGAGGCGCTTTCCTCCGCTCCGCGCCGACCTGCTCCGCTGCGGAGACGCT 120  
DB 1398 TCTGACGAGGCGCTTTCCTCCGCTCCGCGCCGACCTGCTCCGCTGCGGAGACGCT 1457  
QY 121 CGTGTGAGCCCTTATGTGACCTTTGCTGATTTTACCGCCCTGAGAGCGTGAACATGCG 180  
DB 1458 CGTGTGAGCCCTTATGTGACCTTTGCTGATTTTACCGCCCTGAGAGCGTGAACATGCG 1517  
QY 181 GAGCAGAGCGTGTGACAGCACCG 204  
DB 1518 GAGCAGAGCGTGTGACAGCACCG 1541

## RESULT 7

US-09-529-279-1  
Sequence 1, Application US/09529279  
Patent No. 6451617  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT FILING DATE: 2000-04-11  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR APPLICATION NUMBER: JP 9/290188  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1560  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (30)..(1541)  
US-09-529-279-1

Query Match 100.0%; Score 204; DB 3; Length 1560;  
Best Local Similarity 100.0%; Pred. No. 3e-48;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 60  
DB 1338 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 1397  
QY 61 TCTGACGAGGCGCTTTCCTCCGCTCCGCGCCGACCTGCTCCGCTGCGGAGACGCT 120

Db 1398 TCTGACGAGAGGCTCTTCCCTCCGCGCCGCACTCGCTCCGCTGCGAGGAGCGGT 1457  
Qy 121 CGGTGAGGCGCTATGAGACTTTGAGATTATACCGCCCTGGAGCGTGAACATGCG 180  
Db 1458 CGGTGAGGCGCTATGAGACTTTGAGATTATACCGCCCTGGAGCGTGAACATGCG 1517  
Qy 181 GAGCAGAGCGTGTGACAGACCG 204  
Db 1518 GAGCAGAGCGTGTGACAGACCG 1541

## RESULT 8

US-10-158-895-1  
Sequence 1, Application US/10158895  
Patent No. 6551840  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
PRIOR FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1560  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (30)..(1541)  
US-10-158-895-1

Query Match 100.0%; Score 204; DB 4; Length 1560;  
Best Local Similarity 100.0%; Pred. No. 3e-48;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGACGCTCCAGC 60  
Db 1338 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGACGCTCCAGC 1397  
Qy 61 TCTGACGAGAGGCTCTTCCGCTCCGCGCCGCACTGCTCCGCTGCGAGAGCGGT 120  
Db 1398 TCTGACGAGAGGCTCTTCCGCTCCGCGCCGCACTGCTCCGCTGCGAGAGCGGT 1457  
Qy 121 CGGTGAGGCGCTATGAGACTTTGAGATTATACCGCCCTGGAGCGTGAACATGCG 180  
Db 1458 CGGTGAGGCGCTATGAGACTTTGAGATTATACCGCCCTGGAGCGTGAACATGCG 1517  
Qy 181 GAGCAGAGCGTGTGACAGACCG 204  
Db 1518 GAGCAGAGCGTGTGACAGACCG 1541

## RESULT 9

US-09-529-279-42  
Sequence 42, Application US/09529279  
Patent No. 6451617  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/09/529,279

CURRENT FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 42  
LENGTH: 1568  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (11)..(1549)  
US-09-529-279-42

Query Match 100.0%; Score 204; DB 3; Length 1568;  
Best Local Similarity 100.0%; Pred. No. 3e-48;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGACGCTCCAGC 60  
Db 1346 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGACGCTCCAGC 1405  
Qy 61 TCTGACGAGAGGCTCTTCCGCTCCGCGCCGCACTGCTCCGCTGCGAGAGCGGT 120  
Db 1406 TCTGACGAGAGGCTCTTCCGCTCCGCGCCGCACTGCTCCGCTGCGAGAGCGGT 1465  
Qy 121 CGGTGAGGCGCTATGAGACTTTGAGATTATACCGCCCTGGAGCGTGAACATGCG 180  
Db 1466 CGGTGAGGCGCTATGAGACTTTGAGATTATACCGCCCTGGAGCGTGAACATGCG 1525  
Qy 181 GAGCAGAGCGTGTGACAGACCG 204  
Db 1526 GAGCAGAGCGTGTGACAGACCG 1549

## RESULT 10

US-10-158-895-42  
Sequence 42, Application US/10158895  
Patent No. 6551840  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
PRIOR FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 42  
LENGTH: 1568  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (11)..(1549)  
US-10-158-895-42

Query Match 100.0%; Score 204; DB 4; Length 1568;  
Best Local Similarity 100.0%; Pred. No. 3e-48;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGACGCTCCAGC 60  
Db 1346 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGACGCTCCAGC 1405

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QY 61 TCTGACGAGAGCTCTTCCTCCGCGCCGCGCCCACTGCTCCGCTGCGAGAGCGGT 120
DB 1406 TCTGACGAGAGGCTCTTCCTCCGCGCCGCGCCCACTGCTCCGCTGCGAGAGCGGT 1465
QY 121 CGTGTGAGCCCTTATGTGAGACTTGTGAGTTTACCCGCTTGTGAGGCTGAGACCATGCG 180
DB 1466 CGTGTGAGCCCTTATGTGAGACTTGTGAGTTTACCCGCTTGTGAGGCTGAGACCATGCG 1525
QY 181 GAGCAGAGCGTGTGTGACAGACCG 204
DB 1526 GAGCAGAGCGTGTGTGACAGACCG 1549

RESULT 11
US-09-529-279-10
; Sequence 10, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1557)
; US-09-529-279-10

Query Match 100.0%; Score 204; DB 3; Length 1569;
Best Local Similarity 100.0%; Pred. No. 3e-48;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCGACCTTAACTCCCTGACGTCACCAACGACGAGAGCGAGCTTCACG 60
DB 1315 CAAAGCCGACCTTAACTCCCTGACGTCACCAACGACGAGAGCGAGCTTCACG 1374
QY 61 TCTGACGAGAGGCTCTTCCTCCGCGCCGCGCCCACTGCTCCGCTGCGAGAGCGGT 120
DB 1375 TCTGACGAGAGGCTCTTCCTCCGCGCCGCGCCCACTGCTCCGCTGCGAGAGCGGT 1434
QY 121 CGTGTGAGCCCTTATGTGAGACTTGTGAGTTTACCCGCTTGTGAGGCTGAGACCATGCG 180
DB 1435 CGTGTGAGCCCTTATGTGAGACTTGTGAGTTTACCCGCTTGTGAGGCTGAGACCATGCG 1494
QY 181 GAGCAGAGCGTGTGTGACAGACCG 204
DB 1495 GAGCAGAGCGTGTGTGACAGACCG 1518

RESULT 12
US-10-158-895-10
; Sequence 10, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
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; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1557)
; US-10-158-895-10

Query Match 100.0%; Score 204; DB 4; Length 1569;
Best Local Similarity 100.0%; Pred. No. 3e-48;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCGACCTTAACTCCCTGACGTCACCAACGACGAGAGCGAGCTTCACG 60
DB 1315 CAAAGCCGACCTTAACTCCCTGACGTCACCAACGACGAGAGCGAGCTTCACG 1374
QY 61 TCTGACGAGAGGCTCTTCCTCCGCGCCGCGCCCACTGCTCCGCTGCGAGAGAGGT 120
DB 1375 TCTGACGAGAGGCTCTTCCTCCGCGCCGCGCCCACTGCTCCGCTGCGAGAGAGGT 1434
QY 121 CGTGTGAGCCCTTATGTGAGACTTGTGAGTTTACCCGCTTGTGAGGCTGAGACCATGCG 180
DB 1435 CGTGTGAGCCCTTATGTGAGACTTGTGAGTTTACCCGCTTGTGAGGCTGAGACCATGCG 1494
QY 181 GAGCAGAGCGTGTGTGACAGACCG 204
DB 1495 GAGCAGAGCGTGTGTGACAGACCG 1518

RESULT 13
US-09-252-991A-4932/C
; Sequence 4932, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4932
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-4932

Query Match 18.2%; Score 37.2; DB 4; Length 1278;
Best Local Similarity 57.9%; Pred. No. 0.42;
Matches 66; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 64 GACGAGAGGCTCTTCCTCCGCGCCGCGCCCACTGCTCCGCTGCGAGAGAGGTCT 123
DB 691 GACGAGAGGCTCTTCCTCCGCGCCGCGCCCACTGCTCCGCTGCGAGAGAGGTCT 632
QY 124 GTTGAAGCCCTTATGTGAGACTTGTGAGTTTACCCGCTTGTGAGGCTGAGACCAT 177
DB 631 GCGGAGACCGGTCTCGCGCTGTGAGCAGAGCGGACGTCAGTGCAGGCTTAACCTT 578
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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6043.588 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Published Applications NA:\*

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22:	/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
23:	/cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*
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26:	/cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	204	100.0	US-10-123-427-1	Sequence 1, Appl
2	204	100.0	US-10-123-427-5	Sequence 5, Appl
3	204	100.0	US-10-158-895-1	Sequence 1, Appl
4	204	100.0	US-10-384-743-1	Sequence 1, Appl
5	204	100.0	US-10-158-895-12	Sequence 42, Appl
6	204	100.0	US-10-384-743-42	Sequence 42, Appl
7	204	100.0	US-10-158-895-10	Sequence 10, Appl

8	204	100.0	1569	16	US-10-384-743-10	Sequence 10, Appl
9	204	100.0	3095	20	US-10-820-583A-19	Sequence 19, Appl
10	204	100.0	16877	9	US-09-764-877-3349	Sequence 3349, Ap
11	204	100.0	16877	17	US-10-242-515-3349	Sequence 3349, Ap
12	203.6	99.8	636	9	US-09-925-100-330	Sequence 330, App
13	199.2	97.6	409	10	US-09-918-995-32946	Sequence 32946, A
14	40.4	19.8	1455	18	US-10-425-114-28790	Sequence 28790, A
15	40.4	19.8	1458	18	US-10-425-114-28790	Sequence 22226, A
16	40.4	19.8	1486	20	US-10-425-115-80582	Sequence 80582, A
17	38.6	18.9	543	20	US-10-425-115-36239	Sequence 36239, A
18	38.6	18.9	1082	20	US-10-425-115-85134	Sequence 85134, A
19	38.6	18.9	2212	18	US-10-425-114-33344	Sequence 33344, A
20	37.8	18.5	1765	20	US-10-425-114-36243	Sequence 36243, A
21	37.2	18.2	670	17	US-10-264-049-1952	Sequence 1952, Ap
22	36.8	18.0	2036	9	US-09-866-582-17	Sequence 17, Appl
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24	36.4	17.8	531	14	US-10-101-464A-289	Sequence 289, App
25	36.4	17.8	591	21	US-10-864-252-289	Sequence 289, App
26	36.4	17.8	2380	14	US-10-101-464A-864	Sequence 864, App
27	36.4	17.8	2380	21	US-10-864-252-864	Sequence 864, App
28	36.2	17.7	2922	15	US-10-156-761-1749	Sequence 1749, Ap
29	36.2	17.7	138203	21	US-10-819-386A-1	Sequence 1, Appl
30	36.2	17.7	9025608	15	US-10-156-761-1	Sequence 1, Appl
31	36	17.6	4548	19	US-10-437-963-101113	Sequence 101113, A
32	35.6	17.5	2424	17	US-10-282-122A-15037	Sequence 15037, A
33	35.4	17.4	270	19	US-10-437-963-29640	Sequence 29640, A
34	35.4	17.4	975	13	US-10-027-632-10526	Sequence 10526, A
35	35.4	17.4	975	17	US-10-027-632-10526	Sequence 10526, A
36	35.4	17.4	1322	19	US-10-437-963-30124	Sequence 30124, A
37	35.2	17.3	14643	15	US-10-156-761-931	Sequence 931, App
38	35.2	17.3	31422	19	US-10-204-862A-2	Sequence 2, Appl
39	35.2	17.3	31422	24	US-11-005-196-2	Sequence 2, Appl
40	35	17.2	535	19	US-10-437-963-21851	Sequence 21851, A
41	35	17.2	1637	17	US-10-310-154-30	Sequence 30, Appl
42	35	17.2	1637	21	US-10-732-923-164	Sequence 164, App
43	35	17.2	1785	20	US-10-739-930-2060	Sequence 2060, App
44	35	17.2	5811	13	US-10-002-600-15	Sequence 15, Appl
45	34.8	17.1	459	20	US-10-425-115-22523	Sequence 22523, A

#### ALIGNMENTS

RESULT 1  
US-10-123-427-1  
; Sequence 1, Application US/10123427  
; Publication No. US20020119525A1  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/123,427  
FILING DATE: 17-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996

APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1541  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 30..1541  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
IS-10-123-447-1

Query Match	100.0%	Score 204,	DB 13,	Length 1560,
Similarity	100.0%	Pred. No. 6,	2e-53,	
Best Local	0	Mismatches	0,	Indels 0,
Matches 204,	Conservative			Gaps 0,

QY	1	CAAAAGCCGACCTTTAACCCCTGCACTCCACCAACGACACAGCAGAGCAGCAGCTCCAGC	60
Db	1338	CAAAAGCCCGACCTTTAACCCCTGCACTCCACCAACGACACAGCAGAGCAGCAGCTCCAGC	1397
QY	61	TCCTGACGGAAGCCCTTCGCGTCCCGGACCGCCACCTCGCTCCCGCTGGCGAGGAACGCT	120
Db	1398	TCCTGACGGAAGCCCTTCGCGTCCCGGACCGCCACCTCGCTCCCGCTGGCGAGGAACGCT	1457
QY	121	CGTGTGAGGCCCTATGTGACCTTTGTCTGAGATTTTAAACGCGCTCTGGAGACGTTGACCAATGGC	180
Db	1458	CGTGTGAGGCCCTATGTGACCTTTGTCTGAGATTTTAAACGCGCTCTGGAGACGTTGACCAATGGC	1517
QY	181	GAGCAGAGCGTGTGACGACACCG	204
Db	1518	GAGCAGAGCGTGTGACGACACCG	1541

RESULT 2  
 US-10-123-427-5  
 Sequence 5, Application US/10123427  
 Publication No. US20020119525A1  
 GENERAL INFORMATION:  
 APPLICANT: MATSUMOTO, Kunihiko  
 NISHIDA, Eisuke  
 TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSES: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/123,427  
 FILING DATE: 17-Apr-2002  
 CLASSIFICATION: <Unknown>

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SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
S-10-123-427-5

Query	March	Similarity	Score	DB	Length
Best	Local	100.0%	204	13	1560
Matches	Conservative	100.0%	0	6.2e-53	0
				Prid. No.	0
				Mismatches	0
				Indels	0
				Gaps	0
Qy	1	CAAGCCCGACCTTAACTTCAGTCCACCAACGACAGCAGACGAGCAGCTCCAGC	60		
Db	1338	CAAGCCCGACCTTAACTTCAGTCCACCAACGACAGCAGACGAGCAGCTCCAGC	1397		
Qy	61	TCGACCGAGGAGCTCTTCGCTCCCGGCGGACCACTGCTCCGCTGGGAGAGACGGT	120		
Db	1398	TCGACCGAGGAGCTCTTCGCTCCCGGCGGACCACTGCTCCGCTGGGAGAGACGGT	1457		
Qy	121	CGTGTGAGCCCTATGAGACTTGTGAGTTTAAACGGCCCTGGAACCGTGGACCATGAC	180		
Db	1458	CGTGTGAGCCCTATGAGACTTGTGAGTTTAAACGGCCCTGGAACCGTGGACCATGAC	1517		
Qy	181	GAGCAGAGCGTGTGACAGACCG	204		
Db	1518	GAGCAGAGCGTGTGACAGACCG	1541		

RESULT 3  
 US-10-158-895-1  
 ; Sequence 1, Application US/10158895  
 ; Publication No. US20020155624v1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ONO, KOICHIRO  
 ; APPLICANT: ONOTO, TOSHIO  
 ; APPLICANT: TSUCHIYA, MASAYUKI  
 ; TITLE OF INVENTION: METHOD OF SCREENING TGF- $\beta$  INHIBITORY SUBSTANCES  
 ; FILE REFERENCE: 053466/0278  
 ; CURRENT APPLICATION NUMBER: US/10/158, 895  
 ; PRIOR FILING DATE: 2002-06-03  
 ; PRIOR APPLICATION NUMBER: US/09/529, 279  
 ; PRIOR FILING DATE: 2000-04-11  
 ; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
 ; PRIOR FILING DATE: 1998-10-22  
 ; PRIOR APPLICATION NUMBER: JP 9/290188  
 ; PRIOR FILING DATE: 1997-10-22  
 ; NUMBER OF SEQ ID NOS: 48  
 ; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1  
LENGTH: 1560  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (30)..(1541)  
US-10-158-895-1

Query Match 100.0%; Score 204; DB 13; Length 1560;  
Best Local Similarity 100.0%; Pred. No. 6.2e-53;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCGACCTTAACCTTCAGTCCAGCAACGACGACGACGACGACGCTCCAGC 60  
DB 1338 CAAAGCCGACCTTAACCTTCAGTCCAGCAACGACGACGACGACGACGCTCCAGC 1337  
QY 61 TCTGACGAGGAGGCTCTTCCGCTCCGCGCCGACCTCGCTCCGCTGCGGAGAGCGGT 120  
DB 1398 TCTGACGAGGAGGCTCTTCCGCTCCGCGCCGACCTCGCTCCGCTGCGGAGAGCGGT 1457  
QY 121 CGTGTGAGCCCTTAATGAGACTTTGAGTTTACCGGCTCTGAGAGGTGACCAATGCG 180  
DB 1458 CGTGTGAGCCCTTAATGAGACTTTGAGTTTACCGGCTCTGAGAGGTGACCAATGCG 1517  
QY 181 GAGCAGAGCGGTGTGACGACGACCG 204  
DB 1518 GAGCAGAGCGGTGTGACGACGACCG 1541

RESULT 4  
US-10-384-743-1  
Sequence 1, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1560  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (30)..(1541)  
US-10-384-743-1

Query Match 100.0%; Score 204; DB 16; Length 1560;  
Best Local Similarity 100.0%; Pred. No. 6.2e-53;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCGACCTTAACCTTCAGTCCAGCAACGACGACGACGACGACGCTCCAGC 60  
DB 1338 CAAAGCCGACCTTAACCTTCAGTCCAGCAACGACGACGACGACGACGCTCCAGC 1397  
QY 61 TCTGACGAGGAGGCTCTTCCGCTCCGCGCCGACCTCGCTCCGCTGCGGAGAGCGGT 120  
DB 1398 TCTGACGAGGAGGCTCTTCCGCTCCGCGCCGACCTCGCTCCGCTGCGGAGAGCGGT 1457  
QY 121 CGTGTGAGCCCTTAATGAGACTTTGAGTTTACCGGCTCTGAGAGGTGACCAATGCG 180

DB 1458 CGTGTGAGCCCTTAATGAGACTTTGAGTTTACCGGCTCTGAGAGGTGACCAATGCG 1517  
QY 181 GAGCAGAGCGGTGTGACGACGACCG 204  
DB 1518 GAGCAGAGCGGTGTGACGACGACCG 1541

RESULT 5  
US-10-158-895-42  
Sequence 42, Application US/10158895  
Publication No. US20020155624A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 42  
LENGTH: 1568  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (11)..(1549)  
US-10-158-895-42

Query Match 100.0%; Score 204; DB 13; Length 1568;  
Best Local Similarity 100.0%; Pred. No. 6.2e-53;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCGACCTTAACCTTCAGTCCAGCAACGACGACGACGACGACGCTCCAGC 60  
DB 1246 CAAAGCCGACCTTAACCTTCAGTCCAGCAACGACGACGACGACGACGCTCCAGC 1405  
QY 61 TCTGACGAGGAGGCTCTTCCGCTCCGCGCCGACCTCGCTCCGCTGCGGAGAGCGGT 120  
DB 1406 TCTGACGAGGAGGCTCTTCCGCTCCGCGCCGACCTCGCTCCGCTGCGGAGAGCGGT 1465  
QY 121 CGTGTGAGCCCTTAATGAGACTTTGAGTTTACCGGCTCTGAGAGGTGACCAATGCG 180  
DB 1466 CGTGTGAGCCCTTAATGAGACTTTGAGTTTACCGGCTCTGAGAGGTGACCAATGCG 1525  
QY 181 GAGCAGAGCGGTGTGACGACGACCG 204  
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RESULT 6  
US-10-384-743-42  
Sequence 42, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22



;; PRIOR FILING DATE: 2003-04-08  
;; NUMBER OF SEQ ID NOS: 24  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 19  
;; LENGTH: 3095  
;; TYPE: DNA  
;; ORGANISM: HUMAN  
US-10-820-583A-19

Query Match 100.0%; Score 204; DB 20; Length 3095;  
Best Local Similarity 100.0%; Pred. No. 6,4e-53;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGCCGACCTTAACCTTCGAGTCCACCAACGACGACGAGAGAGAGCTCCAGC 60  
DB 1329 CAAGCCGACCTTAACCTTCGAGTCCACCAACGACGACGAGAGAGAGAGCTCCAGC 1388  
QY 61 TCTGACGAGAGGCTCTTCCGCTCCCGGCCGCACTCGCTCCCGCTGAGGAGCGGT 120  
DB 1389 TCTGACGAGAGGCTCTTCCGCTCCCGGCCGCACTCGCTCCCGCTGAGGAGCGGT 1448  
QY 121 CGTGTGAGCCCTTAATGTGACTTTGCTGAGTTTACCGCTCTGAGCGTGGACCATGGC 180  
DB 1449 CGTGTGAGCCCTTAATGTGACTTTGCTGAGTTTACCGCTCTGAGCGTGGACCATGGC 1508  
QY 181 GAGCAGAGCGTGTGACAGCACCG 204  
DB 1509 GAGCAGAGCGTGTGACAGCACCG 1532

## RESULT 10

US-09-764-877-3349  
;; Sequence 3349, Application US/09764877  
;; Patent No. US20020147140A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Rosen et al.  
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
;; FILE REFERENCE: PC005  
;; CURRENT APPLICATION NUMBER: US/09/764,877  
;; PRIOR FILING DATE: 2001-01-17  
;; Prior application data removed - refer to PALM or file wrapper  
;; NUMBER OF SEQ ID NOS: 4031  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 3349  
;; LENGTH: 16877  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-764-877-3349

Query Match 100.0%; Score 204; DB 9; Length 16877;  
Best Local Similarity 100.0%; Pred. No. 6,8e-53;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGCCGACCTTAACCTTCGAGTCCACCAACGACGACGAGAGAGAGCTCCAGC 60  
DB 15011 CAAGCCGACCTTAACCTTCGAGTCCACCAACGACGACGAGAGAGAGAGCTCCAGC 15070  
QY 61 TCTGACGAGAGGCTCTTCCGCTCCCGGCCGCACTCGCTCCCGCTGAGGAGCGGT 120  
DB 15071 TCTGACGAGAGGCTCTTCCGCTCCCGGCCGCACTCGCTCCCGCTGAGGAGCGGT 15130  
QY 121 CGTGTGAGCCCTTAATGTGACTTTGCTGAGTTTACCGCTCTGAGCGTGGACCATGGC 180  
DB 15131 CGTGTGAGCCCTTAATGTGACTTTGCTGAGTTTACCGCTCTGAGCGTGGACCATGGC 15190  
QY 181 GAGCAGAGCGTGTGACAGCACCG 204  
DB 15191 GAGCAGAGCGTGTGACAGCACCG 15214

## RESULT 11

US-10-242-515-3349  
;; Sequence 3349, Application US/10242515

;; Publication No. US20040009488A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Rosen et al.  
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
;; FILE REFERENCE: PC005C1  
;; CURRENT APPLICATION NUMBER: US/10/242,515  
;; PRIOR FILING DATE: 2002-09-13  
;; PRIOR APPLICATION NUMBER: 09/764,877  
;; PRIOR FILING DATE: 2001-01-17  
;; PRIOR APPLICATION NUMBER: 60/179,065  
;; PRIOR FILING DATE: 2000-01-31  
;; PRIOR APPLICATION NUMBER: 60/180,628  
;; PRIOR FILING DATE: 2000-02-04  
;; PRIOR APPLICATION NUMBER: 60/214,886  
;; PRIOR FILING DATE: 2000-06-28  
;; PRIOR APPLICATION NUMBER: 60/217,487  
;; PRIOR FILING DATE: 2000-07-11  
;; PRIOR APPLICATION NUMBER: 60/225,758  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/220,963  
;; PRIOR FILING DATE: 2000-07-26  
;; PRIOR APPLICATION NUMBER: 60/217,496  
;; PRIOR FILING DATE: 2000-07-11  
;; PRIOR APPLICATION NUMBER: 60/225,447  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/218,290  
;; PRIOR FILING DATE: 2000-07-14  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 4031  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 3349  
;; LENGTH: 16877  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-242-515-3349

Query Match 100.0%; Score 204; DB 17; Length 16877;  
Best Local Similarity 100.0%; Pred. No. 6,8e-53;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGCCGACCTTAACCTTCGAGTCCACCAACGACGACGAGAGAGAGCTCCAGC 60  
DB 15011 CAAGCCGACCTTAACCTTCGAGTCCACCAACGACGACGAGAGAGAGAGCTCCAGC 15070  
QY 61 TCTGACGAGAGGCTCTTCCGCTCCCGGCCGCACTCGCTCCCGCTGAGGAGCGGT 120  
DB 15071 TCTGACGAGAGGCTCTTCCGCTCCCGGCCGCACTCGCTCCCGCTGAGGAGCGGT 15130  
QY 121 CGTGTGAGCCCTTAATGTGACTTTGCTGAGTTTACCGCTCTGAGCGTGGACCATGGC 180  
DB 15131 CGTGTGAGCCCTTAATGTGACTTTGCTGAGTTTACCGCTCTGAGCGTGGACCATGGC 15190  
QY 181 GAGCAGAGCGTGTGACAGCACCG 204  
DB 15191 GAGCAGAGCGTGTGACAGCACCG 15214

## RESULT 12

US-09-925-300-330  
;; Sequence 330, Application US/09925300  
;; Patent No. US20020151681A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Craig Rosen,  
;; APPLICANT: Steve Ruben,  
;; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
;; FILE REFERENCE: PA101  
;; CURRENT APPLICATION NUMBER: US/09/925,300  
;; PRIOR FILING DATE: 2000-03-08  
;; PRIOR APPLICATION NUMBER: PCT/US00/05988  
;; PRIOR FILING DATE: 1999-03-12  
;; NUMBER OF SEQ ID NOS: 1890

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: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 330
: LENGTH: 696
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (643)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (657)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (685)
: OTHER INFORMATION: n equals a,t,g, or c
: JS-09-925-300-330

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Query Match	99.8%	Score 203.6;	DB 9;	Length 696;
Best Local Similarity	99.5%	Pred. No. 8.1e-53;		
Matches 203; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	CAAAAGCCCACTTTAACTCTGCAAGTCAACCAACAGCAACAGAGAGGAGGAGCTCCAGC	60
Db	49	CAAAAGCCCACTTTAACTCTGCAAGTCAACCAACAGCAACAGAGAGGAGGAGCTCCAGC	108
QY	61	TTTGACGAGAGCCTCTTCGCTCCCGACCCGACCCTGACCTCCGCTGAGGAGAGCGAT	120
Db	109	TTTACGAGAGCCTCTTCGCTCCCGACCCGACCCTGACCTCCGCTGAGGAGAGCGAT	168
QY	121	CGGTGTGAGCCCTAATGTGACATTTTGTGAGTTTAAACGCTCTTGAGAGGTGAAACATAGC	180
Db	169	CGGTGTGAGCCCTAATGTGACATTTTGTGAGTTTAAACGCTCTTGAGAGGTGAAACATAGC	228
QY	181	GAGCAGAGCGTGTGACAGCAACCG	204
Db	229	GAGCAGAGCGTGTGACAGCAACCG	252

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RESULT 13
US-09-918-995-32946
/ Sequence 32946, Application US/09918995
/ Publication No. US20030073623A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyeq, Inc.
/ TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
/ TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
/ FILE REFERENCE: 20411-756
/ CURRENT APPLICATION NUMBER: US/09/918,995
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: US/09/235,076
/ PRIOR FILING DATE: 1999-01-20
/ NUMBER OF SEQ ID NOS: 38054
/ SOFTWARE: FASTSEQ for Windows Version 3.0
/ SEQ ID NO 32946
/ LENGTH: 409
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-918-995-32946

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Query Match	97.6%	Score 199.2;	DB 10;	Length 409;
Best Local Similarity	98.5%;	Pred. No. 1.8e-51;		
Matches 201; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0

QY 1 CAAAGCCGCACTTAACTCTGCAATCCACCAACGCAACGCAAGACGACGCTCCAGC 60  
Db 48 CAAAGCCGCACTTAACTCTGCAAGCCACCAACAGCAACGCAAGACGACGCTCCAGC 107  
QY 61 TCTGA CGAGAGGCTCTTCCGCTCCCGGACCGCCACTGCTCCCGCTCGCGAGAGAGCT 120  
Db 108 TCTGA CGAGAGGCTCTTCCGCTCCCGGACCGCCACTGCTCCCGCTCGCGAGAGAGCT 167  
QY 121 CGTGTGAACCTTAACTGGACTTTGCTGATTTTACGCGCTCTGAGAGTGAACATGAC 180

Db	168	CGTGTGAGGCCCTCATATGTGACATTTTGCTGAGCTTTACCGCTCTGTGAGCGTGACCATGGC	227
QY	181	GAGCAGAGCGTGTGTGACAGACCG	204
Db	228	GAGCAGAGCGCGGTGACAGACCG	251

RESULT 14  
US-10-425-114-28790/c  
; Sequence 28790, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:

```

/ APPLICANT: Zhou Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ. ID NOS: 73128
/ SEQ ID NO 28790
/ LENGTH: 1455
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB4764-017-F8_FLI
/ US-10-425-114-28790

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Query Match	19.8%;	Score 40.4;	DB 18;	Length 1455;
Best Local Similarity	55.7%;	Pred. No. 0.013;		
Matches 97;	Conservative 0;	Mismatches 76;	Indels 1;	Gaps 1;

Oy	21	GCACTCCACCAACGACGACGACGACAGAGCTCCAGCTCTTACGAGAGGCTCTTCGG	80
Db	1091	GCCTGTGGGCGGTAAAGCTCTGACGACAGGCGCGCTGGCTTCG-CCAACTCTTCTTCGG	1033
Oy	81	CTCCCGGCGCGCCACTCTGCTCCCGCGCTGGCGAGAGCGGTGTGTGAGCCCTTAATGTCGA	140
Db	1032	CCGTGTGCGCGCGCGCGCGCGCGCTGCACTAAGGCGGCGAAAGGGGTGTATTAAAGTTCGAGAGGA	973
Oy	141	CTTGTCTAGTTTATCCGCTCTTGAGCCGTGGAACCATGCGCAGCAGACGCGTGT	194
Db	972	GGAAGTATCGATTTGCGCGGAGTTCAGCCCGCGAGCAGCATGAGAGCGCCGCGT	919

RESULT 15  
US-10-425-114-22226/c  
; Sequence 22226, Application US/10425114  
; Publication No. US20040034888A1

? APPLICANT: Liu, Jingdong  
 ? APPLICANT: Zhou, Yihua  
 ? APPLICANT: Kovalic, David K.  
 ? APPLICANT: Screen, Steven E  
 ? APPLICANT: Tabaska, Jack E  
 ? APPLICANT: Cao, Yongwei  
 ? TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ? TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

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1 CURRENT APPLICATION NUMBER: US-10-0425,114
2 CURRENT FILING DATE: 2003-04-28
3 NUMBER OF SEQ. ID NOS: 73128
4 SEQ. ID NO 22226
5 LENGTH: 1458
6 TYPE: DNA
7 ORGANISM: Zea mays
8 FEATURE:
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10 OTHER INFORMATION: Clone ID: LIB3357-044-G5
11 US-10-0425-114-22226
12

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Query Match 19.8%; Score 40.4; DB 18; Length 1458;  
Best Local Similarity 55.7%; Pred. No. 0.013; Mismatches 1; Gaps 1;  
Matches 97; Conservative 0; Indels 76; Indels 1; Gaps 1;  
QY 21 GCAGTCCACCAACACGACACGACAGCAGCAGCTCCAGCTCTGACGAGGCTCTTCCG 80  
DB 1093 GCCGTCCGCCGCTGAAGCTCTGACAGCAGGCGCGCTCCG-CGAACTCTCTCCG 1035  
QY 81 CTCCTGGGCGCGCCCACTGCTCCCGCTGCGAGAGCGTGTGAGCCCTATGTGA 140  
DB 1034 CCGTCCGCCCGCGCGCGCTGACTAAGCGCGCGAAGGCGGTGTGAGGTGAGGAGA 975  
QY 141 CTTGCTGAGTTTAAACGCTCTGAGCGTGAACATGCGAGCAGAGCGTGT 134  
DB 974 GGAAGTACGGTTGCGCGGTGAGCGCGGAGCAGACTGAGAGCGCGGT 921

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Job time : 223.473 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus.n2p model

Run on: August 2, 2005, 17:28:02 ; Search time 6.66216 Seconds  
(without alignments)  
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Title: US-09-830-144-3\_COPY\_1338\_1541  
Perfect score: 361  
Sequence: 1 caaagccgcagccttaacct.....agaagctgtgtgacagcaccg 204

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Ygapop 10.0 , Ygapext 0.5  
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Minimum DB seq length: 0  
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Maximum Match 100%  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	359	99.4	504	2	US-08-752-891-2
2	359	99.4	504	2	US-08-752-891-6
3	359	99.4	504	2	US-09-144-178-2
4	359	99.4	504	2	US-09-144-178-6
5	359	99.4	504	3	US-09-406-854-2
6	359	99.4	504	3	US-09-406-854-6
7	359	99.4	504	4	US-09-529-279-2
8	359	99.4	504	4	US-10-158-895-2
9	359	99.4	513	4	US-09-529-279-43
10	359	99.4	513	4	US-10-158-895-43
11	359	99.4	517	4	US-09-529-279-11
12	359	99.4	517	4	US-10-158-895-11

13	100.5	27.8	136	4	US-09-252-991A-22734	Sequence 22734, A
C 14	92.5	24.6	189	4	US-09-252-991A-17056	Sequence 17056, A
C 15	89.5	23.8	303	4	US-09-252-991A-19799	Sequence 19799, A
C 16	86.5	23.0	466	4	US-09-252-991A-22592	Sequence 22592, A
C 17	84.5	22.5	353	4	US-09-252-991A-20195	Sequence 20195, A
C 18	84.5	22.3	333	4	US-09-252-991A-20478	Sequence 20478, A
C 19	84	22.3	721	4	US-09-252-991A-28293	Sequence 28293, A
C 20	83.5	22.2	338	4	US-09-252-991A-16820	Sequence 16820, A
C 21	83.5	22.2	480	4	US-09-252-991A-20125	Sequence 20125, A
C 22	83	22.1	264	4	US-09-252-991A-24262	Sequence 24262, A
C 23	82	21.8	269	4	US-09-252-991A-26605	Sequence 26605, A
C 24	81.5	21.7	200	4	US-09-252-991A-19793	Sequence 19793, A
C 25	81.5	21.7	355	4	US-09-252-991A-22326	Sequence 22326, A
C 26	81	21.5	201	4	US-09-252-991A-25745	Sequence 25745, A
C 27	81	21.5	1228	4	US-09-252-991A-17764	Sequence 17764, A
C 28	80.5	21.4	239	4	US-09-252-991A-25387	Sequence 25387, A
C 29	80.5	21.4	589	4	US-09-252-991A-32631	Sequence 32631, A
C 30	80	21.3	338	4	US-09-252-991A-19609	Sequence 19609, A
C 31	79.5	22.0	136	4	US-09-252-991A-23572	Sequence 23572, A
C 32	79	21.0	243	4	US-09-252-991A-26015	Sequence 26015, A
C 33	79	21.0	350	4	US-09-252-991A-19537	Sequence 19537, A
C 34	78.5	20.9	268	4	US-09-252-991A-27950	Sequence 27950, A
C 35	78.5	20.9	297	4	US-09-252-991A-18932	Sequence 18932, A
C 36	78	20.7	416	4	US-09-252-991A-32875	Sequence 32875, A
C 37	78	20.7	297	4	US-09-252-991A-24946	Sequence 24946, A
C 38	77.5	20.6	246	4	US-09-252-991A-23345	Sequence 23345, A
C 39	77.5	20.6	345	4	US-09-252-991A-32325	Sequence 32325, A
C 40	77	21.3	16	4	US-09-529-279-41	Sequence 41, Appl
C 41	77	21.3	16	4	US-10-158-895-41	Sequence 41, Appl
C 42	77	20.5	279	4	US-09-252-991A-26860	Sequence 26860, A
C 43	77	20.5	586	4	US-09-252-991A-28601	Sequence 28601, A
C 44	77	20.5	763	4	US-09-252-991A-30146	Sequence 30146, A
C 45	76.5	21.2	224	4	US-09-252-991A-19251	Sequence 19251, A

#### ALIGNMENTS

RESULT 1  
US-08-752-891-2  
Sequence 2, Application US/08752891  
Patent No. 5837819  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:





FILED DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-406-854-2

Alignment Scores:  
Pred. No.: 4,49e-34 Length: 504  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.45% Indels: 0  
DB: 3 Gaps: 0

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-09-406-854-2 (1-504)

QY 1 CAAAGCCCGACCTTAACCTTCAGTCCACGACGACGACGACGACGACGCTCCAGC 60  
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QY 61 TCTGACGAGGAGGCTCTTCCGCTCCCGGCGCCGACCTGCTCCCGCTGCGAGGAGCGT 120  
Db 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476  
QY 121 CGTGTGAGCCCTATGTGAGACTTTGCTGAGTTTACCGCTCTGAGCGTGAACCATGCG 180  
Db 477 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 496  
QY 181 GAGGAGAGCGGTGGAGACGACGCG 204  
Db 497 GluGlnSerValValThrAlaPro 504

RESULT 6  
US-09-406-854-6  
Sequence 6, Application US/09406854  
Patent No. 6140042  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
APPLICANT: NISHIDA, Eisuke  
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-406-854-6

Alignment Scores:  
Pred. No.: 4,49e-34 Length: 504  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.45% Indels: 0  
DB: 3 Gaps: 0

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Db 437 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 456  
QY 61 TCTGACGAGGAGGCTCTTCCGCTCCCGGCGCCGACCTGCTCCCGCTGCGAGGAGCGT 120  
Db 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476  
QY 121 CGTGTGAGCCCTATGTGAGACTTTGCTGAGTTTACCGCTCTGAGCGTGAACCATGCG 180  
Db 477 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 496  
QY 181 GAGGAGAGCGGTGGAGACGACGCG 204  
Db 497 GluGlnSerValValThrAlaPro 504

RESULT 7  
US-09-529-279-2  
Sequence 2, Application US/09529279  
Patent No. 6451617  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHITAKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/09/529,279  
CURRENT FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 504  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-529-279-2

Alignment Scores:  
Pred. No.: 4,49e-34 Length: 504  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0



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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-43

Alignment Scores:
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Score: 359.00           Matches: 68
Percent Similarity: 100.00% Conservative: 0
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Query Match: 99.45%      Indels: 0
DB: 4                   Gaps: 0

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Db 466 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 485
QY 121 CGGTGTGAGCCCTAATGTGACTTTGCTGAGTTTACCGCTCTGAGCGTGAGCAGCATGGC 180
Db 486 ArgValGluProTyrValAlaAspPheAlaGluPheTyrArgLeuTyrPseValAlaSpHisGly 505
QY 181 GAGCAGAGCGCTGTGACAGCAGCCG 204
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RESULT 11
US-09-529-279-11
; Sequence 11, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529, 279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-279-11

Alignment Scores:
Pred. No.: 4,51e-34      Length: 517
Score: 359.00           Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.45%      Indels: 0
DB: 4                   Gaps: 0

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QY 61 TCTGACGAGGCGCTTCCTCCGCTCCCGGCGCCCACTGCTCCCGCTCCGCTGGGAGAGCGGT 120
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QY 121 CGGTGTGAGCCCTAATGTGACTTTGCTGAGTTTACCGCTCTGAGCGTGAGCAGCATGGC 180
Db 477 ArgValGluProTyrValAlaAspPheAlaGluPheTyrArgLeuTyrPseValAlaSpHisGly 496
QY 181 GAGCAGAGCGCTGTGACAGCAGCCG 204
Db 497 GluGlnSerValValThrAlaPro 504

RESULT 12
US-10-158-895-11
; Sequence 11, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529, 279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-11

Alignment Scores:
Pred. No.: 4,51e-34      Length: 517
Score: 359.00           Matches: 68
Percent Similarity: 100.00% Conservative: 0
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Query Match: 99.45%      Indels: 0
DB: 4                   Gaps: 0

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QY 61 TCTGACGAGGCGCTTCCTCCGCTCCCGGCGCCCACTGCTCCCGCTCCGCTGGGAGAGCGGT 120
Db 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476
QY 121 CGGTGTGAGCCCTAATGTGACTTTGCTGAGTTTACCGCTCTGAGCGTGAGCAGCATGGC 180
Db 477 ArgValGluProTyrValAlaAspPheAlaGluPheTyrArgLeuTyrPseValAlaSpHisGly 496
QY 181 GAGCAGAGCGCTGTGACAGCAGCCG 204
Db 497 GluGlnSerValValThrAlaPro 504

RESULT 13
US-09-252-991A-22734
; Sequence 22734, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
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db 60 ProArgArgArgProGlyGlyArgAlaGlyThrGlyArgSerGlyArg-----

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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Run on: August 2, 2005, 19:59:50 ; Search time 25.2703 Seconds

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6290.398 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5  
Rgapop 6.0 , Rgapext 7.0  
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Searched: 1745140 seqs, 389608008 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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8	359	99.4	517	13	US-10-158-895-11
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26	80.5	21.4	293	15	US-10-425-114-68835
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37	77	21.3	16	13	US-10-158-895-41
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#### ALIGNMENTS

RESULT 1  
US-10-123-427-2

Sequence 2, Application US/10123427  
Publication No. US20020119525A1

GENERAL INFORMATION:

APPLICANT: MATSUMOTO, Kunihiko

NISHIDA, Eisuke

TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESSES:

ADDRESSER: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/123,427  
FILING DATE: 17-APR-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-123-427-2  
  
Alignment Scores:  
Pred. No.: 4,15e-30 Length: 504  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
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DB 437 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 456  
QY 61 TCTGACGAGGAGCTCTCCGCTCCGCGCCGACGACGCTCCGCGCTCCGCGAGACGCT 120  
DB 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476  
QY 121 CGTGTGAGCCCTATGTGACCTTTGCTGACTTTTACCGCTCTGAGCGTGAACATGCG 180  
DB 477 ArgValGluProTyrValAlaPheAlaGluPheTyrArgLeuTrpSerValaAspHisGly 496  
QY 181 GAGCAGAGCGGTGTGACGACGACCG 204  
DB 497 GluGlnSerValValThrAlaPro 504  
  
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US-10-123-427-6  
Sequence 6, Application US/10123427  
Publication No. US20020119525A1  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
NISHIDA, Hisuke  
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/123,427  
FILING DATE: 17-APR-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-123-427-6  
  
Alignment Scores:  
Pred. No.: 4,15e-30 Length: 504  
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QY 61 TCTGACGAGGAGCTCTCCGCTCCGCGCCGACGACGCTCCGCGCTCCGCGAGACGCT 120  
DB 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476  
QY 121 CGTGTGAGCCCTATGTGACCTTTGCTGACTTTTACCGCTCTGAGCGTGAACATGCG 180  
DB 477 ArgValGluProTyrValAlaPheAlaGluPheTyrArgLeuTrpSerValaAspHisGly 496  
QY 181 GAGCAGAGCGGTGTGACGACGACCG 204  
DB 497 GluGlnSerValValThrAlaPro 504  
  
RESULT 3  
US-10-158-895-2  
Sequence 2, Application US/10158895  
Publication No. US20020155624A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
ORTOMO, TOSHITAKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
CURRENT FILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 504  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-2

Alignment Scores:  
Pred. No.: 4.15e-30 Length: 504  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.45% Indels: 0  
DB: 13 Gaps: 0

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DB 437 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 456  
QY 61 TCTGACGAGGAGCTCTTCGCTCCGCGCCGCCCACTGCTCCGCTGGCGAGACGCT 120  
DB 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476  
QY 121 CGGTGAGCCCTATGTCGACTTTGCTGAGTTTACCCCTCTGAGGCTGACCAATGCG 180  
DB 477 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 496  
QY 181 GAGCAGAGCGTGTGACGACGACCG 204  
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RESULT 4  
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Sequence 2, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 504  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-384-743-2

Alignment Scores:  
Pred. No.: 4.15e-30 Length: 504  
Score: 359.00 Matches: 68  
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Query Match: 99.45% Indels: 0  
DB: 14 Gaps: 0

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-10-384-743-2 (1-504)

QY 1 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 60  
DB 437 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 456  
QY 61 TCTGACGAGGAGCTCTTCGCTCCGCGCCGCCCACTGCTCCGCTGGCGAGACGCT 120  
DB 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476  
QY 121 CGGTGAGCCCTATGTCGACTTTGCTGAGTTTACCCCTCTGAGGCTGACCAATGCG 180  
DB 477 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 496  
QY 181 GAGCAGAGCGTGTGACGACGACCG 204  
DB 497 GluGlnSerValValThrAlaPro 504

RESULT 5  
US-10-820-583A-10  
Sequence 10, Application US/10820583A  
Publication No. US20040242461A1  
GENERAL INFORMATION:  
APPLICANT: Schneider, Michael  
APPLICANT: Oh, Hidemasa  
TITLE OF INVENTION: Modulators of Telomere Stability  
FILE REFERENCE: HO-P02673US1  
CURRENT APPLICATION NUMBER: US/10/820,583A  
CURRENT FILING DATE: 2004-04-08  
PRIOR APPLICATION NUMBER: US 60/461,095  
PRIOR FILING DATE: 2003-04-08  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 504  
TYPE: PRT  
ORGANISM: HUMAN  
US-10-820-583A-10

Alignment Scores:  
Pred. No.: 4.15e-30 Length: 504  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.45% Indels: 0  
DB: 16 Gaps: 0

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-10-820-583A-10 (1-504)

QY 1 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 60  
DB 437 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 456  
QY 61 TCTGACGAGGAGCTCTTCGCTCCGCGCCGCCCACTGCTCCGCTGGCGAGACGCT 120  
DB 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476  
QY 121 CGGTGAGCCCTATGTCGACTTTGCTGAGTTTACCCCTCTGAGGCTGACCAATGCG 180  
DB 477 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 496  
QY 181 GAGCAGAGCGTGTGACGACGACCG 204  
DB 497 GluGlnSerValValThrAlaPro 504

RESULT 6  
US-10-158-895-43  
Sequence 43, Application US/10158895  
Publication No. US20020155624A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO

APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 43  
LENGTH: 513  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-43

Alignment Scores:  
Pred. No.: 4.16e-30 Length: 513  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.45% Indels: 0  
DB: 13 Gaps: 0

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-10-158-895-43 (1-513)

QY 1 CAAAGCCGACCTTAACTTCAGTCCAGCAACGACGACGACGACGCTCCAGC 60  
DB 446 GlnSerProThrLeuThrLeuGlnSerThrAsnThrIsthrGlnSerSerSerSer 465  
QY 61 TCTGACGAGGCTCTTCCGCTCCGCGCCGACCTGCTCCGCTGCGAGGACGCT 120  
DB 466 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 485  
QY 121 CGTGTGAGCCCTATGTGACTTTGAGTTTACCGCTTGAGACGTCATGCG 180  
DB 486 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 505  
QY 181 GAGCAGAGCGTGTGACGACGACG 204  
DB 506 GluGlnSerValValThrAlaPro 513

## RESULT 7

US-10-384-743-43  
Sequence 43, Application US/10384743  
Publication No. US2003016228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 43  
LENGTH: 513  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-384-743-43

Alignment Scores:

Pred. No.: 4.16e-30

Length: 513

Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.45% Indels: 0  
DB: 14 Gaps: 0

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-10-384-743-43 (1-513)

QY 1 CAAAGCCGACCTTAACTTCAGTCCAGCAACGACGACGACGACGCTCCAGC 60  
DB 446 GlnSerProThrLeuThrLeuGlnSerThrAsnThrIsthrGlnSerSerSerSer 465  
QY 61 TCTGACGAGGCTCTTCCGCTCCGCGCCGACCTGCTCCGCTGCGAGGACGCT 120  
DB 466 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 485  
QY 121 CGTGTGAGCCCTATGTGACTTTGAGTTTACCGCTTGAGACGTCATGCG 180  
DB 486 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 505  
QY 181 GAGCAGAGCGTGTGACGACGACG 204  
DB 506 GluGlnSerValValThrAlaPro 513

## RESULT 8

US-10-158-895-11  
Sequence 11, Application US/10158895  
Publication No. US20020155624A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 517  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-11

Alignment Scores:  
Pred. No.: 4.16e-30 Length: 517  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.45% Indels: 0  
DB: 13 Gaps: 0

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-10-158-895-11 (1-517)

QY 1 CAAAGCCGACCTTAACTTCAGTCCAGCAACGACGACGACGACGCTCCAGC 60  
DB 437 GlnSerProThrLeuThrLeuGlnSerThrAsnThrIsthrGlnSerSerSerSer 456  
QY 61 TCTGACGAGGCTCTTCCGCTCCGCGCCGACCTGCTCCGCTGCGAGGACGCT 120  
DB 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476  
QY 121 CGTGTGAGCCCTATGTGACTTTGAGTTTACCGCTTGAGACGTCATGCG 180  
DB 477 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 496  
QY 181 GAGCAGAGCGTGTGACGACGACG 204

Db 497 GluGlnSerValValThrAlaPro 504

RESULT 9  
US-10-384-743-11  
Sequence 11, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
PRIOR FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 517  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-384-743-11

Alignment Scores:  
Pred. No.: 4,16e-30 Length: 517  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.45% Indels: 0  
DB: 14 Gaps: 0

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-10-384-743-11 (1-517)

QY 1 CAAAGCCGACCTTAACCTTCAGTCCACCAACAGCAGCAGCAGCAGCAGCTCCAGC 60  
Db 437 GlnSerProThrLeuThrLeuGlnSerThrAsnThrIsthrGlnSerSerSerSer 456  
QY 61 TCTGACGAGGCGCTTTCCTCCGCTCCGCGCCGCCACTGCTCCGCTCCGCGAGACCGT 120  
Db 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476  
QY 121 CGTGTGAGCCCTATGTCGACTTTCGAGTTTTCACCGCCCTCTGAGGCGTGGACCATGCG 180  
Db 477 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 496  
QY 181 GAGCAGACGCTGTGACAGCAGCCG 204  
Db 497 GluGlnSerValValThrAlaPro 504

RESULT 10  
US-09-925-300-1270  
Sequence 1270, Application US/09925300  
Patent No. US20020151681A1  
GENERAL INFORMATION:  
APPLICANT: Steve Ruben,  
APPLICANT: Craig Rosen,  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA101  
CURRENT APPLICATION NUMBER: US/09/925,300  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05988  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1890  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1270

LENGTH: 84  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (38)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-300-1270

Alignment Scores:  
Pred. No.: 1.97e-29 Length: 84  
Score: 352.00 Matches: 67  
Percent Similarity: 98.53% Conservative: 0  
Best Local Similarity: 98.53% Mismatches: 1  
Query Match: 97.51% Indels: 0  
DB: 9 Gaps: 0

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-09-925-300-1270 (1-84)

QY 1 CAAAGCCGACCTTAACCTTCAGTCCACCAACAGCAGCAGCAGCAGCAGCTCCAGC 60  
Db 17 GlnSerProThrLeuThrLeuGlnSerThrAsnThrIsthrGlnSerSerSerSer 36  
QY 61 TCTGACGAGGCGCTTTCCTCCGCTCCGCGCCGCCACTGCTCCGCTCCGCGAGACCGT 120  
Db 37 Ser\*\*\*GlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 56  
QY 121 CGTGTGAGCCCTATGTCGACTTTCGAGTTTTCACCGCCCTCTGAGGCGTGGACCATGCG 180  
Db 57 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 76  
QY 181 GAGCAGACGCTGTGACAGCAGCCG 204  
Db 77 GluGlnSerValValThrAlaPro 84

RESULT 11  
US-10-084-846A-8  
Sequence 8, Application US/10084846A  
Publication No. US20040006026A1  
GENERAL INFORMATION:  
APPLICANT: WEITNAUER, GABRIELE  
APPLICANT: MOHLENWEG, AGNES  
APPLICANT: TREPZER, AXEL  
APPLICANT: BECHTOLD, ANDREAS  
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES  
FILE REFERENCE: 1974-005  
CURRENT APPLICATION NUMBER: US/10/084,846A  
PRIOR FILING DATE: 2003-02-25  
PRIOR APPLICATION NUMBER: PCT/EP01/09815  
PRIOR FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: DE 101 09 166.4  
PRIOR FILING DATE: 2001-02-25  
NUMBER OF SEQ ID NOS: 120  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 8  
LENGTH: 19608  
TYPE: PRT  
ORGANISM: Streptomyces viridochromogenes  
FEATURE:  
OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.  
US-10-084-846A-8

Alignment Scores:  
Pred. No.: 0.179 Length: 19608  
Score: 96.50 Matches: 28  
Percent Similarity: 46.34% Conservative: 10  
Best Local Similarity: 34.15% Mismatches: 21  
Query Match: 25.66% Indels: 23  
DB: 15 Gaps: 5

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-10-084-846A-8 (1-19608)

```

QY      190 CGCTGCTCGCATGGTTCACCGCTCCAGA-----GGCGGTTAA 152
Db      16705 ArgAlaAsnArgSsnGlyProAlaArgArgTrpParArgCysIleuSerProAlaGlyArg 16724
QY      151 ACTGACGAAGTCCACATMGAGGCTCAACACGACCGTCT-----CGC 110
Db      16725 ThrArgSerProAspArgGArgGHIsgLuarProGlyCysCysAlaGlySerArg 16744
QY      109 CAGCGCGGAGCGAGTGGCGCGCGCGGAGCGAAGAGGCGCTCCGTACAGACTGGAAGCTGC 50
Db      16745 ProAlaGlyGlyAlaArgSsnGlyGluAlaGlyArgAlaArgArgArg---ArgCys 16763
QY      49 -----TGCCTGCGCTGTCGCTG-----TGCCTGACTGCAAGG 17
Db      16764 GlyArgGlyProProAlaProCysSerProCysProCysProMetPheGlnThrProGly 16783
QY      16 TTAAG 11
Db      16784 ArgArg 16785

RESULT 12
US-10-425-115-347124
; Sequence 347124, Application US/10425115
; Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 347124
LENGTH: 215
TYPE: prt
ORGANISM: Zea mays
FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_79741C.1.pep
US-10-425-115-347124

Alignment Scores:
Pred. No.:      0.638      Length:      215
Score:          89.50      Matches:      24
Percent Similarity: 45.45%      Conservative: 6
Best Local Similarity: 36.36%      Mismatches: 27
Query Match:      24.79%      Indels:      9
DB:              16      Gaps:      2

US-09-830-144-3_COPY_1338_1541 (1-204) x US-10-425-115-347124 (1-215)
QY      2 AAAGCCGACCTTAAACCTGACAGTCCA-----CCAAACGACACAGCAGAGCAGCA 52
Db      100 ArgProArgProThrProThrProProIleuSerSerProThrArgArgThrArgTrp 119
QY      53 GCTCAGGCTTGACGAGAGGCTCTTCGCTCCCGCGCGCGCCACACTGCTCCGCCCTGAGCG 112.
Db      120 ProProArgSerThrArgCysSerProSerProProProProProArgAla----- 136
QY      113 AGACGCTGCTGTTGAGCTTATGAGACCTTGCTGAGTTTAAACGCTCTGAGAGGTGG 172
Db      137 -----IleIeuSerProThrProThrProThrAlaSerMetSerSerThrCysTrp 153
QY      173 ACCATGGCGAGCAGAGCGC 190
Db      154 ThrArgThrProArgAla 159

RESULT 13
US-10-282-122A-62088
; Sequence 62088, Application US/10282122A
; Publication No. US20040029129A1

```

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/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl
/ APPLICANT: Zykkind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: EITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 62088
/ LENGTH: 245
/ TYPE: PRT
/ ORGANISM: Mycobacterium avium
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (80)..(80)
/ OTHER INFORMATION: x=any amino acid
US-10-282-122A-62088

Alignment Scores:
Pred. No.: 1,21 Length: 245
Score: 87.00 Matches: 29
Percent Similarity: 41.46% Conservative: 5
Best Local Similarity: 35.37% Mismatches: 30
Query Match: 23.14% Indels: 18
DB: 15 Gaps: 5

US-09-830-144_3_COPY_1338_1541 (1-204) x US-10-282-122A-62088 (1-245)
QY 196 TCACACAGCTCT-----GCTCGCATGCTCCACAGCTCCAGAGC 158
D 101 SerProArgSerThrProArgProProthrhSerProthrhSerProthrhProArgSerThSer 120
QY 157 -----GTTAAACTCAGCAAGTCCATATGGGCTCAACAGCAGCGTCTCGCGCAGGCG 104
D 121 TrpIleAlaSerThrThrhArgSerProArgSerGlyProAlaThrProArgProSer 140
QY 103 GGAGCGAGTGGGCGGCGCGGAGCGGAGAGAGGCTCCGCT-----CAGAGCTGG 56
D 141 ArgAlaSerSerSerIleSerThrIleSerThrIleProAlaIleAlaGlySerSerTrp 160
QY 55 -----AGTGTGCTGC-----TCTGCGTGTGCGGTGTGGTGAGCTGAGGAGGTTAAG 11

```



Db 161 ProGlySerCysSerThrProProAlaThrCysArgCysTrpCysThrProProThArg 180  
QY 10 TCGGCGC 5  
Db 181 SerGly 182

## RESULT 14

US-10-437-963-121108  
; Sequence 121108, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Mu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbaruk, Brad  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 121108  
; LENGTH: 588  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: clone ID: PAT\_MRT4530\_24165C.1.pep  
US-10-437-963-121108

## Alignment Scores:

Pred. No.:	1.7	Length:	588
Score:	86.00	Matches:	21
Percent Similarity:	52.31%	Conservative:	13
Best Local Similarity:	32.31%	Mismatches:	23
Query Match:	22.87%	Indels:	8
DB:	16	Gaps:	2

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-10-437-963-121108 (1-588)

QY 196 TCACCAAGCTCTGCTGCGCATGCTCCACGCTCCAGA-----GGCGGTAA 152  
Db 312 ThrProArgAlaAlaSerProSerProArgAlaArgAspValSerIleAlaIleGlyAla 331  
QY 151 ACTCAGCAAGTCCACATAGGAGCTCACAACGACCTCTCCGACGAGCGGAGCGAGTGG 92  
Db 332 SerArgValAlaProProPrometSerSerSerSerArgGlnAlaProAlaSerGly 351  
QY 91 CGGCGCGGAGCGGAGGAGGCTCCGTCAGAGCTGAGCTGCTGCTGCGGTCGTCGT 32  
Db 352 LysGlnSerArgGlyAngIleAla-----AlaAlaSerThrAlaIleGlnArg 368  
QY 31 TGTGACTGCAGG 17  
Db 369 TrpArgSerAlaGly 373

## RESULT 15

US-10-767-701-60458  
; Sequence 60458, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 60458  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: clone ID: 8089004.pep  
US-10-767-701-60458

Alignment Scores:			
Pred. No.:	1.86	Length:	128
Score:	85.00	Matches:	27
Percent Similarity:	45.21%	Conservative:	6
Best Local Similarity:	36.99%	Mismatches:	24
Query Match:	22.61%	Indels:	16
DB:	16	Gaps:	5

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-10-767-701-60458 (1-128)

QY 196 TCACCAAGCTCTGCTGCGCATGCTCCACG-----TCAGAGCGGTAAACT 149  
Db 13 SerProArg-----ArgArgGlyProArgArgArgThrArgGlyCysProArg 30  
QY 148 CAGCAAGTCCACATAGGAGCTCACAACGACCT-----CTCGCCAGGCG 104  
Db 31 ArgGlnHeProSerArgGlyArgArgSerSerGlnPheArgProValProArgArgCys 50  
QY 103 GAGACG--AGTGGCGCGGCGGAGCGGAGGAGGCTCCGTCAGAGCTGAGCTGCTGC 47  
Db 51 GlySerArgGlyGlyArgGlnGlyProAlaArgSerLeuGly-----Cys 66  
QY 46 TGTGCGTGTGCTGTGTGAGCTGCAAGGTTAGTGC 8  
Db 67 ProAlaCysGlyCysArgTrpProArgTrpSerArgSer 79

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Job time : 31.2703 secs

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OM protein - protein search, using SW model

Run on: August 2, 2005, 20:15:38 ; Search time 8.27027 Seconds  
(without alignments)  
613.781 Million cell updates/sec

Title: US-09-830-144-4\_COPY\_437\_504

Perfect score: 359 1 QSTFTLTIQSTINTHTQSSSS.....AEFYRLMSVDHGQSVYTPA 68

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PTCUS.COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	359	100.0	504	2	US-08-752-891-2 Sequence 2, Appli
2	359	100.0	504	2	US-08-752-891-6 Sequence 6, Appli
3	359	100.0	504	2	US-09-144-178-2 Sequence 2, Appli
4	359	100.0	504	2	US-09-144-178-6 Sequence 6, Appli
5	359	100.0	504	3	US-09-406-854-2 Sequence 2, Appli
6	359	100.0	504	3	US-09-406-854-6 Sequence 6, Appli
7	359	100.0	504	4	US-09-529-279-2 Sequence 2, Appli
8	359	100.0	504	4	US-10-158-895-2 Sequence 2, Appli
9	359	100.0	513	4	US-09-529-279-43 Sequence 43, Appli
10	359	100.0	513	4	US-10-158-895-43 Sequence 43, Appli
11	359	100.0	517	4	US-09-529-279-11 Sequence 11, Appli
12	359	100.0	517	4	US-10-158-895-11 Sequence 11, Appli
13	77	21.4	16	4	US-09-529-279-41 Sequence 41, Appli
14	77	21.4	16	4	US-10-158-895-41 Sequence 41, Appli
15	75.5	21.0	691	4	US-09-902-540-16476 Sequence 16476, A
16	67.5	18.8	752	4	US-09-919-039-235 Sequence 235, App
17	67.5	18.8	852	2	US-09-070-060-3 Sequence 3, Appli
18	67.5	18.8	852	2	US-09-357-746-3 Sequence 3, Appli
19	66.5	18.5	425	4	US-09-248-796A-14511 Sequence 14511, A
20	66	18.4	16	4	US-09-529-279-40 Sequence 40, Appli
21	66	18.4	16	4	US-10-158-895-40 Sequence 40, Appli
22	65.5	18.2	498	4	US-10-037-667-5 Sequence 5, Appli
23	65	18.1	335	4	US-09-252-991A-24494 Sequence 24494, A
24	64.5	18.0	244	4	US-09-461-325-463 Sequence 463, App
25	64.5	18.0	244	4	US-10-012-542-463 Sequence 463, App
26	64.5	18.0	244	4	US-10-115-123-463 Sequence 463, App
27	63.5	17.7	240	4	US-09-152-060-100 Sequence 100, App

28	63.5	17.7	335	4	US-09-152-060-64 Sequence 64, Appli
29	63.5	17.7	331	3	US-08-706-216-6 Sequence 6, Appli
30	63.5	17.7	391	4	US-09-650-284B-6 Sequence 6, Appli
31	63	17.5	850	4	US-09-915-181A-3 Sequence 3, Appli
32	62	17.3	541	4	US-09-538-092-347 Sequence 347, App
33	62	17.3	602	4	US-09-248-796A-16684 Sequence 16684, A
34	62	17.3	737	4	US-09-583-110-4038 Sequence 4038, Ap
35	62	17.3	742	4	US-09-107-433-3626 Sequence 3626, Ap
36	61	17.0	448	4	US-09-248-796A-14116 Sequence 14116, A
37	61	17.0	522	4	US-09-248-796A-14121 Sequence 14121, A
38	60.5	16.9	854	2	US-09-070-060-4 Sequence 4, Appli
39	60.5	16.9	854	3	US-09-357-746-4 Sequence 4, Appli
40	60	16.7	642	4	US-09-248-796A-16106 Sequence 16106, A
41	60	16.7	1037	4	US-09-428-711A-21 Sequence 21, Appli
42	58.5	16.3	1060	4	US-09-248-796A-16624 Sequence 16624, A
43	58.5	16.3	1093	3	US-08-545-860D-55 Sequence 55, Appli
44	58.5	16.3	1093	5	PCT-US94-04496-55 Sequence 55, Appli
45	58.5	16.3	3256	4	US-09-919-172-98 Sequence 98, Appli

#### ALIGNMENTS

RESULT 1  
US-08-752-891-2  
Sequence 2, Application US/08752891  
Patent No. 5837819  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
APPLICANT: NISHIDA, Eisuke  
TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-752-891-2  
Query Match 100.0%; Score 359; DB 2; Length 504;  
Best Local Similarity 100.0%; Pred. No. 4.6e-37;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 QSPFLTIGSTNTHHTQSSSSSDGGLFRSRPAHSLPFGEDGVRVEPYVDFAEFYRLMSVDHG 60
Db 437 QSPFLTIGSTNTHHTQSSSSSDGGLFRSRPAHSLPFGEDGVRVEPYVDFAEFYRLMSVDHG 496
OY 61 EQSVVTAP 68
Db 497 EQSVVTAP 504

RESULT 2
US-08-752-891-6
; Sequence 6, Application US/08752891
; Patent No. 5837819
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiko
; APPLICANT: NISHIDA, Eisuke
; TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; City: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,891
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-752-891-6

Query Match 100.0%; Score 359; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 4.6e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QSPFLTIGSTNTHHTQSSSSSDGGLFRSRPAHSLPFGEDGVRVEPYVDFAEFYRLMSVDHG 60
Db 437 QSPFLTIGSTNTHHTQSSSSSDGGLFRSRPAHSLPFGEDGVRVEPYVDFAEFYRLMSVDHG 496
OY 61 EQSVVTAP 68
Db 497 EQSVVTAP 504

RESULT 3
US-09-144-178-2
; Sequence 2, Application US/09144178

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/ Patent No. 5989862
/ GENERAL INFORMATION:
/ APPLICANT: MATSUMOTO, Kunihiko
/ APPLICANT: NISHIDA, Eisuke
/ TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Foley & Lardner
/ STREET: 3000 K Street, N.W., Suite 500
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20007-5109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/144,178
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/752,891
/ FILING DATE: 20-NOV-1996
/ APPLICATION NUMBER: JP 8-300856
/ FILING DATE: 28-OCT-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 8-126282
/ FILING DATE: 24-APR-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 17981/111
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 504 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-144-178-2

Query Match      100.0%; Score 359; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 4,6e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Cy      1 QSPFTLLOSTNTHHTOSSSSSDGGLFSRPAHSLPPEEDGRVPPYDFAEFRLMSVDHG 60
      |||||||
Db      437 QSPFTLLOSTNTHHTOSSSSSDGGLFSRPAHSLPPEEDGRVPPYDFAEFRLMSVDHG 496
      |||||||

Gy      61 EGSVVTAP 68
      |||||||
Db      497 EGSVVTAP 504

RESULT 4
US-09-144-178-6
/ Sequence 6, Application US/09144178
/ Patent No. 5989862
/ GENERAL INFORMATION:
/ APPLICANT: MATSUMOTO, Kunihiko
/ APPLICANT: NISHIDA, Eisuke
/ TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Foley & Lardner
/ STREET: 3000 K Street, N.W., Suite 500
/ CITY: Washington
/ STATE: D.C.

```

COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,178  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-144-178-6

Query Match 100.0%; Score 359; DB 2; Length 504;  
Best Local Similarity 100.0%; Pred. No. 4.6e-37;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTQSTNTHVTHQSSSSSDGGLFRSRPAHSILPPGSDGVEPYVDAEFYRLMSVDHG 60  
DB 437 QSPFTLTQSTNTHVTHQSSSSSDGGLFRSRPAHSILPPGSDGVEPYVDAEFYRLMSVDHG 496  
QY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 5  
US-09-406-854-2  
Sequence 2, Application US/09406854  
Patent No. 6140042  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihito  
APPLICANT: NISHIDA, Eisuke  
TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-406-854-2

Query Match 100.0%; Score 359; DB 3; Length 504;  
Best Local Similarity 100.0%; Pred. No. 4.6e-37;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTQSTNTHVTHQSSSSSDGGLFRSRPAHSILPPGSDGVEPYVDAEFYRLMSVDHG 60  
DB 437 QSPFTLTQSTNTHVTHQSSSSSDGGLFRSRPAHSILPPGSDGVEPYVDAEFYRLMSVDHG 496  
QY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 6  
US-09-406-854-6  
Sequence 6, Application US/09406854  
Patent No. 6140042  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihito  
APPLICANT: NISHIDA, Eisuke  
TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 504 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-854-6

Query Match

Best Local Similarity 100.0%; Score 359; DB 3; Length 504;  
Pred. No. 4.6e-37;

Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAFYRLMSVDHG 60

DB 437 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAFYRLMSVDHG 496

QY 61 EQSVVTAP 68

DB 497 EQSVVTAP 504

RESULT 7

US-09-529-279-2

Sequence 2, Application US/09529279

Patent No. 6451617

GENERAL INFORMATION:

APPLICANT: ONO, KOICHIRO

APPLICANT: OHTOMO, TOSHIHIKO

APPLICANT: TSUCHIYA, MASAYUKI

TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES

FILE REFERENCE: 053466/0278

CURRENT APPLICATION NUMBER: US/09/529,279

PRIOR FILING DATE: 2000-04-11

PRIOR APPLICATION NUMBER: PCT/JP98/04796

PRIOR FILING DATE: 1998-10-22

PRIOR APPLICATION NUMBER: JP 9/290188

PRIOR FILING DATE: 1997-10-22

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 504

TYPE: PRT

ORGANISM: Homo sapiens

US-09-529-279-2

Query Match

Best Local Similarity 100.0%; Score 359; DB 4; Length 504;  
Pred. No. 4.6e-37;

Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAFYRLMSVDHG 60

DB 437 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAFYRLMSVDHG 496

QY 61 EQSVVTAP 68

DB 497 EQSVVTAP 504

RESULT 8

US-10-158-895-2

Sequence 2, Application US/10158895

Patent No. 6551840

GENERAL INFORMATION:

APPLICANT: ONO, KOICHIRO

APPLICANT: OHTOMO, TOSHIHIKO

APPLICANT: TSUCHIYA, MASAYUKI

TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES

FILE REFERENCE: 053466/0278

CURRENT APPLICATION NUMBER: US/10/158,895

CURRENT FILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: US/09/529,279

PRIOR FILING DATE: 2000-04-11

PRIOR APPLICATION NUMBER: PCT/JP98/04796

PRIOR FILING DATE: 1998-10-22

PRIOR APPLICATION NUMBER: JP 9/290188

PRIOR FILING DATE: 1997-10-22

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 504

TYPE: PRT

ORGANISM: Homo sapiens

US-10-158-895-2

Query Match

Best Local Similarity 100.0%; Score 359; DB 4; Length 504;  
Pred. No. 4.6e-37;

Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAFYRLMSVDHG 60

DB 437 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAFYRLMSVDHG 496

QY 61 EQSVVTAP 68

DB 497 EQSVVTAP 504

RESULT 9

US-09-529-279-43

Sequence 43, Application US/09529279

Patent No. 6451617

GENERAL INFORMATION:

APPLICANT: ONO, KOICHIRO

APPLICANT: OHTOMO, TOSHIHIKO

APPLICANT: TSUCHIYA, MASAYUKI

TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES

FILE REFERENCE: 053466/0278

CURRENT APPLICATION NUMBER: US/09/529,279

PRIOR FILING DATE: 2000-04-11

PRIOR APPLICATION NUMBER: PCT/JP98/04796

PRIOR FILING DATE: 1998-10-22

PRIOR APPLICATION NUMBER: JP 9/290188

PRIOR FILING DATE: 1997-10-22

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 43

LENGTH: 513

TYPE: PRT

ORGANISM: Homo sapiens

US-09-529-279-43

Query Match

Best Local Similarity 100.0%; Score 359; DB 4; Length 513;  
Pred. No. 4.7e-37;

Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 EQSVVTAP 68

DB 506 EQSVVTAP 513

RESULT 10

US-10-158-895-43

Sequence 43, Application US/10158895

Patent No. 6551840

GENERAL INFORMATION:

APPLICANT: ONO, KOICHIRO

APPLICANT: OHTOMO, TOSHIHIKO

APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 43  
LENGTH: 513  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-43

Query Match 100.0%; Score 359; DB 4; Length 513;  
Best Local Similarity 100.0%; Pred. No. 4.7e-37;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 446 QSPFLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGDDGRVEPYVDFAEFYRLMSVDHG 505  
OY 61 EOSVVTAP 68  
DB 506 EOSVVTAP 513

RESULT 11  
US-09-529-279-11  
Sequence 11, Application US/09529279  
Patent No. 6451617  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/09/529,279  
CURRENT FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 517  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-529-279-11

Query Match 100.0%; Score 359; DB 4; Length 517;  
Best Local Similarity 100.0%; Pred. No. 4.7e-37;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QSPFLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGDDGRVEPYVDFAEFYRLMSVDHG 60  
DB 437 QSPFLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGDDGRVEPYVDFAEFYRLMSVDHG 496  
OY 61 EOSVVTAP 68  
DB 497 EOSVVTAP 504

RESULT 12  
US-10-158-895-11  
Sequence 11, Application US/10158895  
Patent No. 6551640

GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 517  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-11

Query Match 100.0%; Score 359; DB 4; Length 517;  
Best Local Similarity 100.0%; Pred. No. 4.7e-37;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QSPFLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGDDGRVEPYVDFAEFYRLMSVDHG 60  
DB 437 QSPFLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGDDGRVEPYVDFAEFYRLMSVDHG 496  
OY 61 EOSVVTAP 68  
DB 497 EOSVVTAP 504

RESULT 13  
US-09-529-279-41  
Sequence 41, Application US/09529279  
Patent No. 6451617  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/09/529,279  
CURRENT FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 41  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-529-279-41

Query Match 21.4%; Score 77; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0027;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QSPFLTQSTNTHTQ 15  
DB 2 QSPFLTQSTNTHTQ 16

RESULT 14  
US-10-158-895-41

; Sequence 41, Application US/10158895  
; Patent No. 6551840  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHIHIKO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/10/158,895  
; PRIOR FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: US/09/529,279  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: JP 9/290188  
; PRIOR FILING DATE: 1997-10-22  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-158-895-41

Query Match 21.4%; Score 77; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0027;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPPLTQSTNTHTQ 15  
Db 2 QSPPLTQSTNTHTQ 16

RESULT 15  
US-09-902-540-16476  
; Sequence 16476, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 16476  
; LENGTH: 691  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-16476

Query Match 21.0%; Score 75.5; DB 4; Length 691;  
Best Local Similarity 29.0%; Pred. No. 0.61;  
Matches 18; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

QY 5 LTLQSTNTHTQSSSSSDGLFRSRPAHSILPFGDGRVEPYVDFAEFYRLMSVDHGQSV 64  
Db 420 VTMERLNVHARGCVLWTKMKATDYEDLPFGAGRVNDFVLYVERIRA-AIEHQQLAN 478  
QY 65 VT 66  
Db 479 VT 480



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OM protein - protein search, using sw model

Run on: August 2, 2005, 20:29:48 ; Search time 25.0405 Seconds

(without alignments)  
1058.018 Million cell updates/sec

Title: US-09-830-144-4\_COPY\_437\_504

Perfect score: 359  
Sequence: 1 QSTPLTQSTNTHTQSSSSS.....AEFRYLMVHGEGSVYTP 68

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
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- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	359	100.0	504	13	US-10-123-427-2
2	359	100.0	504	13	US-10-123-427-6
3	359	100.0	504	13	US-10-158-895-2
4	359	100.0	504	14	US-10-158-895-2
5	359	100.0	504	16	US-10-820-583A-10
6	359	100.0	513	13	US-10-158-895-43
7	359	100.0	513	13	US-10-384-743-43
8	359	100.0	517	13	US-10-158-895-11
9	359	100.0	517	14	US-10-384-743-11
10	352	98.1	84	9	US-09-925-300-1270
11	77	21.4	16	13	US-10-158-895-41

12	77	21.4	16	14	US-10-384-743-41	Sequence 41, Appl
13	75.5	21.0	64	15	US-10-369-493-19278	Sequence 19278, A
14	70.5	19.6	87	15	US-10-425-115-271372	Sequence 271372, A
15	70	19.5	147	15	US-10-424-599-225143	Sequence 225143, A
16	70	19.4	238	16	US-10-437-963-119398	Sequence 119398, A
17	69.5	19.5	199	9	US-09-941-831-21	Sequence 21, Appl
18	68.5	19.1	213	16	US-10-425-115-305401	Sequence 305401, A
19	67.5	18.8	739	14	US-10-097-534-10	Sequence 10, Appl
20	67.5	18.8	739	15	US-10-374-979-89	Sequence 89, Appl
21	67.5	18.8	739	15	US-10-182-936A-89	Sequence 89, Appl
22	67.5	18.8	739	16	US-10-477-238A-668	Sequence 668, App
23	67.5	18.8	739	17	US-10-680-287A-668	Sequence 668, App
24	67.5	18.8	739	16	US-10-477-173-668	Sequence 668, App
25	67.5	18.8	752	10	US-09-919-039-235	Sequence 235, App
26	67.5	18.8	903	17	US-10-489-740-145	Sequence 145, App
27	67	18.7	170	16	US-10-767-701-61071	Sequence 61071, A
28	66	18.4	16	13	US-10-158-895-40	Sequence 40, Appl
29	66	18.4	16	14	US-10-384-743-40	Sequence 40, Appl
30	65.5	18.2	498	18	US-10-037-667-5	Sequence 5, Appl1
31	65.5	18.2	498	13	US-10-885-227-44	Sequence 44, Appl1
32	64.5	18.0	244	14	US-10-012-542-463	Sequence 463, App
33	64.5	18.0	244	14	US-10-115-123-463	Sequence 463, App
34	64.5	18.0	244	18	US-10-800-834-463	Sequence 463, App
35	63.5	17.7	240	9	US-09-853-161-100	Sequence 100, App
36	63.5	17.7	240	9	US-09-852-659A-100	Sequence 100, App
37	63.5	17.7	240	15	US-10-058-993-100	Sequence 100, App
38	63.5	17.7	240	15	US-10-058-993-100	Sequence 100, App
39	63.5	17.7	335	9	US-09-853-161-64	Sequence 64, Appl
40	63.5	17.7	335	9	US-09-852-659A-64	Sequence 64, Appl
41	63.5	17.7	335	9	US-09-852-659A-64	Sequence 64, Appl
42	63.5	17.7	335	15	US-10-058-993-64	Sequence 64, Appl
43	63.5	17.7	824	14	US-10-226-844-1	Sequence 1, Appl1
44	63.5	17.7	824	14	US-10-210-951-58	Sequence 58, Appl
45	63.5	17.7	824	14	US-10-211-884-58	Sequence 58, Appl

#### ALIGNMENTS

RESULT 1  
US-10-123-427-2  
; Sequence 2, Appl  
; Application US/10123427  
; Publication No. US20020119525A1  
; GENERAL INFORMATION:  
; APPLICANT: MATSUMOTO, Kunihito  
; NISHIDA, Eisuke  
; TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/123,427  
; FILING DATE: 17-Apr-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/406,854  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US/08/752,891  
; FILING DATE: 20-NOV-1996  
; APPLICATION NUMBER: JP 8-300856  
; FILING DATE: 28-OCT-1996  
; APPLICATION NUMBER: JP 8-126282  
; FILING DATE: 24-APR-1996

ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-123-427-2

Query Match 100.0%; Score 359; DB 13; Length 504;  
Best Local Similarity 100.0%; Pred. No. 3.3e-34;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTQSTNTHQTSSSSSDGGLFRSPAHSLPPGEDGRVPEYVDFAEFYRLMSVDHG 60  
DB 437 QSPFTLTQSTNTHQTSSSSSDGGLFRSPAHSLPPGEDGRVPEYVDFAEFYRLMSVDHG 496  
QY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 2  
US-10-123-427-6  
Sequence 6, Application US/10123427  
Publication No. US20020119525A1  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
NISHIDA, Eisuke  
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/123,427  
FILING DATE: 17-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-123-427-6

Query Match 100.0%; Score 359; DB 13; Length 504;  
Best Local Similarity 100.0%; Pred. No. 3.3e-34;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTQSTNTHQTSSSSSDGGLFRSPAHSLPPGEDGRVPEYVDFAEFYRLMSVDHG 60  
DB 437 QSPFTLTQSTNTHQTSSSSSDGGLFRSPAHSLPPGEDGRVPEYVDFAEFYRLMSVDHG 496  
QY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 3  
US-10-158-895-2  
Sequence 2, Application US/10158895  
Publication No. US20020155624A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 2  
LENGTH: 504  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-2

Query Match 100.0%; Score 359; DB 13; Length 504;  
Best Local Similarity 100.0%; Pred. No. 3.3e-34;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTQSTNTHQTSSSSSDGGLFRSPAHSLPPGEDGRVPEYVDFAEFYRLMSVDHG 60  
DB 437 QSPFTLTQSTNTHQTSSSSSDGGLFRSPAHSLPPGEDGRVPEYVDFAEFYRLMSVDHG 496  
QY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 4  
US-10-384-743-2  
Sequence 2, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279

PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 504  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-384-743-2

Query Match  
Best Local Similarity 100.0%; Score 359; DB 14; Length 504;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLQSTNTHTQSSSSSDGGLFRSRPAHSLPPGDDGVEPYVDFAEFRRLMSVDHG 60  
DB 437 QSPFTLQSTNTHTQSSSSSDGGLFRSRPAHSLPPGDDGVEPYVDFAEFRRLMSVDHG 496

QY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 5  
US-10-820-583A-10  
Sequence 10, Application US/10820583A  
Publication No. US20040242461A1  
GENERAL INFORMATION:  
APPLICANT: Schneider, Michael  
TITLE OF INVENTION: Modulators of Telomere Stability  
FILE REFERENCE: HO-P02673US1  
CURRENT APPLICATION NUMBER: US/10/820,583A  
PRIOR FILING DATE: 2004-04-08  
PRIOR APPLICATION NUMBER: US 60/461,095  
PRIOR FILING DATE: 2003-04-08  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 504  
TYPE: PRT  
ORGANISM: HUMAN  
US-10-820-583A-10

Query Match  
Best Local Similarity 100.0%; Score 359; DB 16; Length 504;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLQSTNTHTQSSSSSDGGLFRSRPAHSLPPGDDGVEPYVDFAEFRRLMSVDHG 60  
DB 437 QSPFTLQSTNTHTQSSSSSDGGLFRSRPAHSLPPGDDGVEPYVDFAEFRRLMSVDHG 496

QY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 6  
US-10-158-895-43  
Sequence 43, Application US/10158895  
Publication No. US20020155624A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIIKO  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279

PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 43  
LENGTH: 513  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-43

Query Match  
Best Local Similarity 100.0%; Score 359; DB 13; Length 513;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLQSTNTHTQSSSSSDGGLFRSRPAHSLPPGDDGVEPYVDFAEFRRLMSVDHG 60  
DB 446 QSPFTLQSTNTHTQSSSSSDGGLFRSRPAHSLPPGDDGVEPYVDFAEFRRLMSVDHG 505

QY 61 EQSVVTAP 68  
DB 506 EQSVVTAP 513

RESULT 7  
US-10-384-743-43  
Sequence 43, Application US/10384743  
Publication No. US2003016228A1  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, TOSHIIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
PRIOR FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 43  
LENGTH: 513  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-384-743-43

Query Match  
Best Local Similarity 100.0%; Score 359; DB 14; Length 513;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLQSTNTHTQSSSSSDGGLFRSRPAHSLPPGDDGVEPYVDFAEFRRLMSVDHG 60  
DB 446 QSPFTLQSTNTHTQSSSSSDGGLFRSRPAHSLPPGDDGVEPYVDFAEFRRLMSVDHG 505

QY 61 EQSVVTAP 68  
DB 506 EQSVVTAP 513

RESULT 8  
US-10-158-895-11  
Sequence 11, Application US/10158895  
Publication No. US20020155624A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIIKO  
APPLICANT: TSUCHIYA, MASAYUKI

;; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
;; FILE REFERENCE: 053466/0278  
;; CURRENT APPLICATION NUMBER: US/10/158,895  
;; PRIOR FILING DATE: 2002-06-03  
;; PRIOR APPLICATION NUMBER: US/09/529,279  
;; PRIOR FILING DATE: 2000-04-11  
;; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: PCT/US00/05988  
;; PRIOR FILING DATE: 1997-10-22  
;; NUMBER OF SEQ ID NOS: 48  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 11  
;; LENGTH: 517  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-158-895-11

Query Match 100.0%; Score 359; DB 13; Length 517;  
Best Local Similarity 100.0%; Pred. No. 3.4e-34;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGVEPYVDFAEFFRLMSVDHG 60  
DB 437 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGVEPYVDFAEFFRLMSVDHG 496  
OY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 9  
US-10-384-743-11  
;; Sequence 11, Application US/10384743  
;; Publication No. US2003016228A1  
;; GENERAL INFORMATION:  
;; APPLICANT: ONO, KOICHIRO  
;; APPLICANT: OHTOMO, TOSHIHIKO  
;; APPLICANT: TSUCHIYA, MASAYUKI  
;; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
;; FILE REFERENCE: 053466/0278  
;; CURRENT APPLICATION NUMBER: US/10/384,743  
;; CURRENT FILING DATE: 2003-03-11  
;; PRIOR APPLICATION NUMBER: US/09/529,279  
;; PRIOR FILING DATE: 2000-04-11  
;; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: JP 9/290188  
;; PRIOR FILING DATE: 1997-10-22  
;; NUMBER OF SEQ ID NOS: 48  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 11  
;; LENGTH: 517  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-384-743-11

Query Match 100.0%; Score 359; DB 14; Length 517;  
Best Local Similarity 100.0%; Pred. No. 3.4e-34;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGVEPYVDFAEFFRLMSVDHG 60  
DB 437 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGVEPYVDFAEFFRLMSVDHG 496  
OY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 10  
US-09-925-300-1270  
;; Sequence 1270, Application US/09925300

;; Patent No. US20020151681A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Craig Rosen,  
;; APPLICANT: Steve Ruben,  
;; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
;; FILE REFERENCE: PA101  
;; CURRENT APPLICATION NUMBER: US/09/925,300  
;; CURRENT FILING DATE: 2001-08-10  
;; PRIOR APPLICATION NUMBER: PCT/US00/05988  
;; PRIOR FILING DATE: 2000-03-08  
;; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
;; PRIOR FILING DATE: 1997-10-22  
;; NUMBER OF SEQ ID NOS: 1890  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 1270  
;; LENGTH: 84  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: SITE  
;; LOCATION: (38)  
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-300-1270

Query Match 98.1%; Score 352; DB 9; Length 84;  
Best Local Similarity 98.5%; Pred. No. 2.6e-34;  
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGVEPYVDFAEFFRLMSVDHG 60  
DB 17 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGVEPYVDFAEFFRLMSVDHG 76  
OY 61 EQSVVTAP 68  
DB 77 EQSVVTAP 84

RESULT 11  
US-10-158-895-41  
;; Sequence 41, Application US/10158895  
;; Publication No. US20020155624A1  
;; GENERAL INFORMATION:  
;; APPLICANT: ONO, KOICHIRO  
;; APPLICANT: OHTOMO, TOSHIHIKO  
;; APPLICANT: TSUCHIYA, MASAYUKI  
;; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
;; FILE REFERENCE: 053466/0278  
;; CURRENT APPLICATION NUMBER: US/10/158,895  
;; CURRENT FILING DATE: 2002-06-03  
;; PRIOR APPLICATION NUMBER: US/09/529,279  
;; PRIOR FILING DATE: 2000-04-11  
;; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: JP 9/290188  
;; PRIOR FILING DATE: 1997-10-22  
;; NUMBER OF SEQ ID NOS: 48  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 41  
;; LENGTH: 16  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: Peptide  
US-10-158-895-41

Query Match 21.4%; Score 77; DB 13; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 QSPFTLTQSTNTHTQ 15  
DB 2 QSPFTLTQSTNTHTQ 16

RESULT 12  
US-10-384-743-41  
; Sequence 41, Application US/10384743  
; Publication No. US20030162228A1  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHIMIRO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/10/384,743  
; CURRENT FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: US/09/529,279  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: JP 9/290188  
; PRIOR FILING DATE: 1997-10-22  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-384-743-41

Query Match 21.4%; Score 77; DB 14; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QSPPLTQSTNTHQ 15  
DB 2 QSPPLTQSTNTHQ 16

RESULT 13  
US-10-369-493-19278  
; Sequence 19278, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 19278  
; LENGTH: 641  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-10-369-493-19278

Query Match 21.0%; Score 75.5; DB 15; Length 641;  
Best Local Similarity 29.0%; Pred. No. 4.1;  
Matches 18; Conservative 13; Mismatches 30; Indels 1; Gaps 1;  
QY 5 LTLQSTNTHQSSSSSSDGLFRSPAHSLPPGEGRVEPYVDFAFYRLMSVDHGEOSV 64  
DB 418 VTMLNTHANGEGVTLVTVMKKATDYEDLPFGAGARVWDVFLVERRA-AYEHGQLAN 476  
QY 65 VT 66

DB 477 VT 478  
RESULT 14  
US-10-425-115-271372  
; Sequence 271372, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 271372  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_179086C.1.pep  
US-10-425-115-271372

Query Match 19.6%; Score 70.5; DB 16; Length 87;  
Best Local Similarity 32.3%; Pred. No. 1.5;  
Matches 21; Conservative 4; Mismatches 19; Indels 21; Gaps 3;  
QY 7 LQSTNTHQSSSSSSDGLFRSPAHSLP-----PGEDGRVEPYVD 47  
DB 5 LAAENTH--QAQGBGRRLHILFRRTKSTYPLHWRDWTGKAPSTDGAPVYV 62  
QY 48 FAEFY 52  
DB 63 LAFY 67

RESULT 15  
US-10-424-599-225143  
; Sequence 225143, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 225143  
; LENGTH: 147  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_45334C.1.pep  
US-10-424-599-225143

Query Match 19.5%; Score 70; DB 15; Length 147;  
Best Local Similarity 29.9%; Pred. No. 3.2;  
Matches 23; Conservative 8; Mismatches 24; Indels 22; Gaps 3;  
QY 3 PTLTQSTNTHQSSSSSSDGLFRSPAHSLPPGED-----GRVEY 45  
DB 11 PTLTFLGRSNNNNSSSSAASRIEHRFRIISAMSTPGSSSDSASTKTRVYIKGRVQ-- 68  
QY 46 VDFAEFYRLMSVDHGEQ 62

Wed Aug 3 09:50:51 2005

us-09-830-144-4\_copy\_437\_504.rapb

Page 6

Db 69 ---GVFYNWTFIENATQ 82

Search completed: August 2, 2005, 20:42:13  
Job time : 25.0405 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 2, 2005, 20:33:39 ; Search time 68.4595 Seconds  
(without alignments)  
1625.295 Million cell updates/sec

Title: US-09-830-144-4\_COPY\_437\_504  
Perfect score: 359  
Sequence: 1 QSTPLTILQSTNTHTQSSSS.....AEFRRLMSVDHGQSVYTP 68

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-O/cgn2\_1/USPTO.spool/US09830144/runat 02082005.101155.12556/app.query.fasta\_1.654  
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdd  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=Pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=Pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USBR=US09830144 @CGN 1 1 219 @runat 02082005.101155.12556 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEOUTERY -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -MAIN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database : Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*\n2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*\n3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*\n4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*\n5: /cgn2\_6/ptodata/1/ina/PTUS.COMB.seq:\*\n6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	359	100.0	1560	2	US-08-752-891-1
2	359	100.0	1560	2	US-08-752-891-5
3	359	100.0	1560	2	US-09-144-178-1
4	359	100.0	1560	2	US-09-144-178-5
5	359	100.0	1560	2	US-09-406-854-1
6	359	100.0	1560	3	US-09-406-854-5
7	359	100.0	1560	3	US-09-529-279-1
8	359	100.0	1560	4	US-10-158-895-1
9	359	100.0	1568	4	US-09-529-279-42
10	359	100.0	1568	4	US-10-158-895-42
11	359	100.0	1569	3	US-09-529-279-10
12	359	100.0	1569	4	US-10-158-895-10

13	75.5	21.0	2076	4	US-09-902-540-9325	Sequence 9325, App
14	75.5	21.0	9839	4	US-09-902-540-996	Sequence 996, App
15	71.5	19.9	1108	5	PCT-US93-03035-1	Sequence 1, Appli
16	69	19.2	44998	4	US-09-949-016-12824	Sequence 12824, A
17	69	19.2	44999	4	US-09-949-016-14832	Sequence 14832, A
18	69	19.2	44999	4	US-09-949-016-14833	Sequence 14833, A
19	69	19.2	44999	4	US-09-949-016-17109	Sequence 17109, A
20	69	19.2	44999	4	US-09-949-016-17109	Sequence 17109, A
21	68	18.9	146307	4	US-09-949-016-14881	Sequence 14881, A
22	68	18.9	146307	4	US-09-949-016-14882	Sequence 14882, A
23	68	18.9	146307	4	US-09-949-016-14883	Sequence 14883, A
24	68	18.9	146307	4	US-09-949-016-14884	Sequence 14884, A
25	68	18.9	146307	4	US-09-949-016-14885	Sequence 14885, A
26	68	18.9	146307	4	US-09-949-016-12836	Sequence 12836, A
27	68	18.9	146307	4	US-09-949-016-12837	Sequence 12837, A
28	68	18.9	146307	4	US-09-949-016-14888	Sequence 14888, A
29	68	18.9	148405	4	US-09-949-016-11747	Sequence 11747, A
30	68	18.9	148405	4	US-09-949-016-12835	Sequence 12835, A
31	68	18.9	148405	4	US-09-949-016-12836	Sequence 12836, A
32	68	18.9	148405	4	US-09-949-016-12837	Sequence 12837, A
33	67.5	18.8	2559	2	US-09-070-060-2	Sequence 2, Appli
34	67.5	18.8	2559	3	US-09-357-746-2	Sequence 234, App
35	67.5	18.8	2678	4	US-09-919-039-234	Sequence 1, Appli
36	67.5	18.8	5359	2	US-09-070-060-1	Sequence 15731, A
37	67.5	18.8	5372	3	US-09-357-746-1	Sequence 15731, A
38	67	18.7	19161	4	US-09-949-016-15731	Sequence 15731, A
39	67	18.7	42894	4	US-09-949-016-12301	Sequence 12301, A
40	67	18.7	42898	4	US-09-949-016-15904	Sequence 15904, A
41	66.5	18.5	1275	4	US-09-248-796A-408	Sequence 408, App
42	66	18.4	601	4	US-09-949-016-56557	Sequence 56557, A
43	66	18.4	601	4	US-09-949-016-59181	Sequence 59181, A
44	66	18.4	43537	4	US-09-949-016-13458	Sequence 13458, A
45	66	18.4	636591	4	US-09-949-016-11808	Sequence 11808, A

#### ALIGNMENTS

RESULT 1  
US-08-752-891-1  
; Sequence 1, Application US/08752891  
; Patent No. 5837819  
; GENERAL INFORMATION:  
; APPLICANT: MATSUMOTO, Kunihiko  
; APPLICANT: NISHIDA, Rikaue  
; TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSER: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/752,891  
; FILING DATE: 20-NOV-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 8-300856  
; FILING DATE: 28-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 8-126282  
; FILING DATE: 24-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 17981/111  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1541  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 30..1541  
US-08-752-891-1

Alignment Scores:  
Pred. No.: 3,91e-37 Length: 1560  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 2

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-08-752-891-1 (1-1560)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20  
DB 1338 CAAAGCCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 1397

QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGlyAspGly 40  
DB 1398 TCTGACGAGGCGCTTCCGCTCCCGGCCCACTCGCTCCGCTGCGGAGAGAGGT 1457

QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60  
DB 1458 CGGTGAGCCCTTAAGTGAAGTTTACCGGCTCTGAGAGCGTGAACATGG 1517

QY 61 GluGlnSerValValThrAlaPro 68  
DB 1518 GAGCAGAGCGTGTGACGACGACCG 1541

RESULT 2  
US-08-752-891-5  
Sequence 5, Application US/08752891  
Patent No. 5837819  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
APPLICANT: NISHIDA, Eisuke  
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282

FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1541  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 30..1541  
US-08-752-891-5

Alignment Scores:  
Pred. No.: 3,91e-37 Length: 1560  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 2

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-08-752-891-5 (1-1560)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20  
DB 1338 CAAAGCCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGCTCCAGC 1397

QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGlyAspGly 40  
DB 1398 TCTGACGAGGCGCTTCCGCTCCCGGCCCACTCGCTCCGCTGCGGAGAGAGGT 1457

QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60  
DB 1458 CGGTGAGCCCTTAAGTGAAGTTTACCGGCTCTGAGAGCGTGAACATGG 1517

QY 61 GluGlnSerValValThrAlaPro 68  
DB 1518 GAGCAGAGCGTGTGACGACGACCG 1541

RESULT 3  
US-09-144-178-1  
Sequence 1, Application US/09144178  
Patent No. 5989862  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
APPLICANT: NISHIDA, Eisuke  
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,178  
FILING DATE:



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1 CLASSIFICATION:
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: US 08/752,891
4 FILING DATE: 20-NOV-1996
5 APPLICATION NUMBER: JP 8-300856
6 FILING DATE: 28-OCT-1996
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: JP 8-126282
9 FILING DATE: 24-APR-1996
10 ATTORNEY/AGENT INFORMATION:
11 NAME: BENT, Stephen A.
12 REGISTRATION NUMBER: 29,768
13 REFERENCE/DOCKET NUMBER: 17981/11111
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: (202)672-5300
16 TELEFAX: (202)672-5399
17 TELEX: 904136
18 INFORMATION FOR SEQ ID NO: 1:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 1560 base pairs
21 TYPE: nucleic acid
22 STRANDEDNESS: double
23 TOPOLOGY: linear
24 FEATURE:
25 NAME/KEY: CDS
26 LOCATION: 30..1541
27 FEATURE:
28 NAME/KEY: mat_peptide
29 LOCATION: 30..1541
30 US-09-144-178-1

```

Alignment Scores:	
Pred. No.:	3.91e-37
Score:	359.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	2
Length:	1560
Matches:	68
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-830-144-4\_COPY\_437\_504 (1-68) X US-09-144-178-1 (1-1560)

QY	1	GINserProthrlLeuThrLeuGInserThraLeuTrhIstYrInGInserSerSerSerSer	20
Db	1338	CANAAGCCGACCTTAAACCTCGACGTCACCAACGACGACGACGACGACGCTCCAGC	1397
QY	21	SerAEPGLYGLYLeuPheArgSerArgProAlaHisSerLeuProProGlnuAspLys	40
Db	1388	TCTGACGAGAGCCTTTCCGCTCCCGGCGCCGACCTGCTCCCGCTGGCGAGGACGGT	1457
QY	41	ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly	60
Db	1458	CGTGTGAGCCCTATGTGGACCTTTCCTAGTTTACCCCTCTGGAGCGGTGACCATGCG	1517
QY	61	GluGInserValValThrAlaPro	68
Db	1518	GAGCAGAGCGGTGACAGCACCG	1541

RESULT 4  
 US-09-144-178-5  
 ; Sequence 5, Application US/09144178  
 ; Patent No. 5989862  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MATSUMOTO, Kunihito  
 ; APPLICANT: NISHIDA, Eisuke  
 ; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,178
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,891
FILING DATE: 20-NOV-1996
APPLICATION NUMBER: JP 8-300856
FILING DATE: 28-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-126282
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 17981/111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 30..1541
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 30..1541
US-09-144-178-5

Alignment Scores:
Pied. No.: 3,91e-37 Length: 1560
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatch: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-830-144-4_COPY_437_504 (1-68) x US-09-144-178-5 (1-1560)
QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
DB 1338 CAAGGCCGAGCTTAACTTCGACATCCACCAACGACAGCAGACGAGCTCCAGC 1397
QY 21 SerApglyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40
DB 1398 TCTACGAGAGCGCTCTTCCTCCGCTCCGCGCCGCCACCTCGCTCCGCGGAGAGCGGT 1457
QY 41 ArgValGluProGlyTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60
DB 1458 CGGTGTGAGCCCTTAAGTGGACTTTCGAGTTTAACTCCCTTCGAGCGCTGAGCGTGAACATGCG 1517
QY 61 GluGlnSerValValThrAlaPro 68
DB 1518 GAGCAGAGCGGTGTGACAGCAGCG 1541

RESULT 5
US-09-406-854-1
; Sequence 1, Application US/09406854
; Patent No. 6140042
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiko
; APPLICANT: NISHIDA, Risaue
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR

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```

Alignment Scores:
Pred. No.: 3,91e-37 Length: 1560
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-830-144-4_COPY_437_504 (1-68) x US-09-144-178-5 (1-1560)

QY 1 GluSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
1338 CAAGGCCGACCTTAACTTCAGTCCACCAACGACAGCAGCAGCAGCAGCTCCGAC 1397
Db

QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGlyAspGly 40
1398 TCTACGAGAGCCCTCTCCGCTCCCGGCGCCGACCTCGCTCCGCGGAGAGAGCGT 1457
Db

QY 41 ArgValGluProGlyrValAspPheAlaGluPheTyrArgLeuTTPSerValAspHisGly 60
1458 CGGTGTAGCCCTTAAGTGAGACTTTTGCTGAGTTTAAAGCCCTCTGGAGCGTGACCAATGC 1517
Db

QY 61 GluGlnSerValValThrAlaPro 68
1518 GAGCAGAGCGGTGTGACAGCAGCG 1541
Db

RESULT 5
US-09-406-854-1
; Sequence 1, Application US/09406854
; Patent No. 6140042
; GENERAL INFORMATION:
APPLICANT: MATSUMOTO, Kunihiko
APPLICANT: NISHIDA, Risaue
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR

```

NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1541  
NAME/KEY: mat\_peptide  
LOCATION: 30..1541  
US-09-406-854-1  
Alignment Scores:  
Pred. No.: 3.91e-37 Length: 1560  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
US-09-830-144-4\_COPY\_437\_504 (1-68) x US-09-406-854-1 (1-1560)  
QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisEthGlnSerSerSerSer 20  
Db 1338 CAAAGCCCACTTAACCTTCGACGTCCACCAACGACACGAGGACGAGCTTCACG 1397  
QY 21 SerAepGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGlnAepGly 40  
Db 1398 TCTGACGAGGAGCTCTCCGCTCCGCGCCGACCTCGCTCCGCGTGGCAGACGGT 1457  
QY 41 ArgValGlnProThrValAepPheAlaGluPheThrArgLeuThrSerValAepHisGly 60  
Db 1458 CGTGTGACCCCATATGTGACCTTGTCTGAGTTTACCGCTCTGAGCGTGGACCATGAC 1517  
QY 61 GlnGlnSerValValThrAlaPro 68  
Db 1518 GAGCAGAGCGGTGTGACACGACCG 1541

RESULT 6  
US-09-406-854-5  
Sequence 5, Application US/09406854  
Patent No. 6140042  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihito  
TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1541  
NAME/KEY: mat\_peptide  
LOCATION: 30..1541  
US-09-406-854-5  
Alignment Scores:  
Pred. No.: 3.91e-37 Length: 1560  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
US-09-830-144-4\_COPY\_437\_504 (1-68) x US-09-406-854-5 (1-1560)  
QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisEthGlnSerSerSerSer 20  
Db 1338 CAAAGCCCACTTAACCTTCGACGTCCACCAACGACACGAGGACGAGCTTCACG 1397  
QY 21 SerAepGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGlnAepGly 40  
Db 1398 TCTGACGAGGAGCTCTCCGCTCCGCGCCGACCTCGCTCCGCGTGGCAGACGGT 1457





PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 1569  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (7)..(1557)  
US-10-158-895-10

Alignment Scores:  
Pred. No.: 3,94e-37 Length: 1569  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-158-895-10 (1-1569)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSer 20  
DB 1315 CAAAGCCGAGCCTTAACCTGCACTCCACCAACGACGACGACGACGACGCTCCAGC 1374

QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGlyAlaAspGly 40  
DB 1375 TCTGACGAGGAGGCTCTTCCGCTCCGCGCCGCCCACTGCTCCGCTCGGAGAGAGCGT 1434

QY 41 ArgValGluProTyrValAlaAspPheAlaGluPheTyrArgLeuTrpSerValAlaAspHisGly 60  
DB 1435 CGGTTTGAGCCCTATGTGAGCTTGTGAGATTGATTTACCGCTCTGAGAGGTGACCATGAGC 1494

QY 61 GluGlnSerValValThrAlaPro 68  
DB 1495 GAGCAGAGCGGTGTGACAGACCG 1518

RESULT 13  
US-09-902-540-9325  
Sequence 9325, Application US/09902540  
Patent No. 6833447  
GENERAL INFORMATION:  
APPLICANT: Goldman, Barry S.  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Wiegand, Roger C.  
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
FILE REFERENCE: 38-10(15849)B  
CURRENT APPLICATION NUMBER: US/09/902,540  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,883  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 9325  
LENGTH: 2076  
TYPE: DNA  
ORGANISM: Myxococcus xanthus  
US-09-902-540-9325

Alignment Scores:  
Pred. No.: 6.12 Length: 2076  
Score: 75.50 Matches: 18  
Percent Similarity: 50.00% Conservative: 13  
Best Local Similarity: 29.03% Mismatches: 30  
Query Match: 21.03% Indels: 1  
DB: 4 Gaps: 1

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-09-902-540-9325 (1-2076)

QY 5 LeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSerSerSerSerSer 24

DB 1258 GTGACGATGAGAGCGCTGAACGTCCAGCGCGGAGGCGCTCACGCGTGTGACGGTG 1317  
QY 25 LeuPheArgSerArgProAlaHisSerLeuProGlyGlyAlaAspGlyArgValAlaPro 44  
DB 1318 ATGAGAAAGGCCACCGACTACGAGACCTGCGCGCGGAGCGCGGCGGATGATGAGC 1377  
QY 45 TyrValAspPheAlaGluPheTyrArgLeuTrpSerValAlaAspHisGlyGlnGlnSerVal 64  
DB 1378 TTGCTGAGCCTGTGTGAGAGCGCTACCGGCC---GCGTACAGACGACGCGCATGTTGGCCAAC 1434

QY 65 ValThr 66  
DB 1435 GTGACG 1440

RESULT 14  
US-09-902-540-996  
Sequence 996, Application US/09902540  
Patent No. 6833447  
GENERAL INFORMATION:  
APPLICANT: Goldman, Barry S.  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Wiegand, Roger C.  
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
FILE REFERENCE: 38-10(15849)B  
CURRENT APPLICATION NUMBER: US/09/902,540  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,883  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 996  
LENGTH: 9839  
TYPE: DNA  
ORGANISM: Myxococcus xanthus  
US-09-902-540-996

Alignment Scores:  
Pred. No.: 51.3 Length: 9839  
Score: 75.50 Matches: 18  
Percent Similarity: 50.00% Conservative: 13  
Best Local Similarity: 29.03% Mismatches: 30  
Query Match: 21.03% Indels: 1  
DB: 4 Gaps: 1

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-09-902-540-996 (1-9839)

QY 5 LeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSerSerSerSerSer 24

DB 6427 GTGACGATGAGAGCGCTGAACGTCCAGCGCGGAGGCGCTCACGCGTGTGACGGTG 6486

QY 25 LeuPheArgSerArgProAlaHisSerLeuProGlyGlyAlaAspGlyArgValAlaPro 44

DB 6487 ATGAGAAAGGCCACCGACTACGAGACCTGCGCGCGGAGCGCGGCGGATGATGAGC 6546

QY 45 TyrValAspPheAlaGluPheTyrArgLeuTrpSerValAlaAspHisGlyGlnGlnSerVal 64

DB 6547 TTGCTGAGCCTGTGTGAGAGCGCTACCGGCC---GCGTACAGACGACGCGCATGTTGGCCAAC 6603

QY 65 ValThr 66  
DB 6604 GTGACG 6609

RESULT 15  
PCT-US93-03035-1/C  
Sequence 1, Application PC/TUS9303035  
GENERAL INFORMATION:  
APPLICANT: ABBOTT LABORATORIES  
TITLE OF INVENTION: PURIFIED THERMOSTABLE ENDONUCLEASE  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES  
STREET: D-377 APED, ONE ABBOTT PARK ROAD

```

CITY: ABBOTT PARK
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03035
FILING DATE: 19930330
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/869,306
FILING DATE: 16-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/860,702
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: BRAINARD, THOMAS D
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5145.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-4884
TELEFAX: 708-937-2623
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1108 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 114..926
PCT-US93-03035-1

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Alignment Scores:
Pred. No.:      8.64      Length:      1108
Score:          71.50     Matches:      15
Percent Similarity: 70.37% Conservative: 4
Best Local Similarity: 55.56% Mismatches: 7
Query Match:      19.92% Indels:      1
DB:               5      Gaps:      1

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US-09-830-144-4\_COPY\_437\_504 (1-68) x PCT-US93-03035-1 (1-1108)

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QY      18 SerSerSerSerApGlyLeuPheArgSerArgProLahisSerLeuProProGly 37
      |||  ::::|  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      203 AGCGGTGAGGCGCGAGGCGGCTGCTCTCCACCGCCCGGCCACCGCCTTTTCCCGGC 144
QY      38 GIUApGlyArgValGluPro 44
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      143 --GATGAAAGGTGGAACCC 126

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Search completed: August 2, 2005, 20:47:30  
 Job time : 74.4595 sec

GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus.p2n model

Run on: August 2, 2005, 20:40:24 ; Search time 252.243 Seconds

(without alignments)  
1744.825 Million cell updates/secTitle: US-09-830-144-4\_COPY\_437\_504  
Perfect score: 359  
Sequence: 1 QSTPLTLQSTNTHTQSSSS.....AEFYRLMSVDHGHSVTPAR 68Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

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-Q=/cgn2\_1/USPTO.spool/US09830144/funat\_02082005\_101156\_12592/app.query.fasta\_1.654  
-DB=Published Applications NA -OPMT=fastlap -SUFFIX=p2n.rnpb -MINMATCH=0.1  
-LOOPCL=0 -LIMITS-bits -START=1 -END=-1 -MATRIX=blomsum62  
-TRANS=human40.cdi -LIST=45 -DLOCAL=200 -THR\_SCORE=pcr -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFILE=ptc -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US09830144@cgn 1 1 1041@funat\_02082005\_101156\_12592  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEBUFFER -NEG\_SCORES=0 -WAIT -DSELOCK=100  
-LONGIO=0 -DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Published Applications NA.\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_NEW\_PUB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
20: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
21: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
22: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*  
24: /cgn2\_6/ptodata/1/pubpna/US11A\_NEW\_PUB.seq.\*  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	359	100.0	1560	13	US-10-123-427-1	Sequence 1, Appli
2	359	100.0	1560	13	US-10-123-427-5	Sequence 5, Appli
3	359	100.0	1560	13	US-10-158-895-1	Sequence 1, Appli
4	359	100.0	1560	16	US-10-384-743-1	Sequence 1, Appli
5	359	100.0	1560	13	US-10-158-895-42	Sequence 42, Appli
6	359	100.0	1560	16	US-10-384-743-42	Sequence 42, Appli
7	359	100.0	1560	13	US-10-158-895-10	Sequence 10, Appli
8	359	100.0	1560	16	US-10-384-743-10	Sequence 10, Appli
9	359	100.0	3095	20	US-10-820-583A-19	Sequence 19, Appli
10	359	100.0	16877	9	US-09-764-877-3349	Sequence 3349, Ap
11	359	100.0	16877	17	US-10-242-515-3349	Sequence 3349, Ap
12	352	98.1	696	9	US-09-925-100-330	Sequence 330, App
13	346	96.4	409	10	US-09-918-995-32946	Sequence 32946, A
14	346	96.4	409	20	US-10-425-115-151890	Sequence 151890,
15	75.5	21.0	672	10	US-09-928-267-16	Sequence 16, Appli
16	75.5	21.0	833	10	US-09-928-267-8	Sequence 8, Appli
17	75.5	21.0	1923	17	US-10-369-493-42965	Sequence 42965, A
18	75	20.9	301	20	US-10-425-115-43033	Sequence 43033, A
19	75	20.9	1610	10	US-09-971-392-119	Sequence 119, App
20	73	20.3	1536	13	US-10-087-192-1532	Sequence 1532, Ap
21	72	20.1	1405	20	US-10-739-930-2095	Sequence 2095, Ap
22	72	20.1	1917	18	US-10-425-112-127016	Sequence 27016, A
23	72	20.1	2325	20	US-10-425-115-176747	Sequence 176747,
24	71.5	19.9	1797	20	US-10-425-115-79466	Sequence 79466, A
25	71.5	19.9	2616	20	US-10-425-115-79469	Sequence 79469, A
26	71	19.8	996	9	US-09-974-300-6219	Sequence 6219, Ap
27	71	19.8	48829	13	US-10-087-192-1531	Sequence 1531, Ap
28	70.5	19.6	504	20	US-10-425-115-86709	Sequence 86709, A
29	70	19.5	797	18	US-10-425-115-82301	Sequence 82301, A
30	70	19.5	1101	19	US-10-437-963-16915	Sequence 16915, A
31	69.5	19.4	1492	9	US-09-941-831-7	Sequence 7, Appli
32	69.5	19.4	9507	10	US-09-764-891-9785	Sequence 9785, Ap
33	69	19.2	1820	19	US-10-437-963-60665	Sequence 60665, A
34	69	19.2	2745	17	US-10-282-112-13446	Sequence 13446, A
35	69	19.2	12409	10	US-09-989-442-156	Sequence 156, App
36	68.5	19.1	778	20	US-10-425-115-120738	Sequence 120738,
37	68.5	19.1	1373	20	US-10-425-115-139192	Sequence 139192,
38	68.5	19.1	1539	17	US-10-369-493-40524	Sequence 40524, A
39	68.5	19.1	1554	21	US-10-886-906-53	Sequence 53, Appli
40	68.5	19.1	3068	15	US-10-259-453-1	Sequence 1, Appli
41	68.5	19.1	3082	15	US-10-259-453-2	Sequence 2, Appli
42	68.5	19.1	16951	19	US-10-181-1748-72	Sequence 72, Appli
43	68.5	19.1	32767	17	US-10-004-113-4	Sequence 4, Appli
44	68.5	19.1	32767	16	US-10-394-948-4	Sequence 4, Appli
45	68	18.9	273	9	US-09-864-761-22569	Sequence 22569, A

## ALIGNMENTS

RESULT 1  
US-10-123-427-1  
; Sequence 1, Application US/10123427  
; Publication No. US20020119525A1  
; GENERAL INFORMATION:  
; APPLICANT: MATSUMOTO, Kunihito  
; NISHIDA, Eisuke  
; TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/123,427  
FILING DATE: 17-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-Nov-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-Oct-1996  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-Apr-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1541  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 30..1541  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-123-427-1  
Alignment Scores:  
Pred. No.: 4.69e-41 Length: 1560  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0  
US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-123-427-1 (1-1560)  
QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20  
DB 1338 CAAAGCCGACCTTAACCTGCACTGCAACCAACGACGACGACGACGACGACGACG 1397  
QY 21 SerAspGlyIleuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40  
DB 1398 TCTGACGAGGCGCTCTCCGCTCCGCGCCGCGCCGCGCCGCTCCGCTCCGCGCGT 1457  
QY 41 ArgValGluProGlyTrpValaPheAlaGluPheTrpArgLeuTrpSerValaAspHisGly 60  
DB 1458 CGGTGAGGCCCTTAATGAGCTTGTGAGTTTACCGCTTGAGGCGGTGACCATGCGC 1517  
QY 61 GlnGlnSerValValThrAlaPro 68  
DB 1518 GAGCAGAGCGGTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1541  
RESULT 2  
US-10-123-427-5  
Sequence 5, Application US/10123427  
Publication No. US20020119525A1  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko

NISHIDA, Eisuke  
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/123,427  
FILING DATE: 17-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-Nov-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-Oct-1996  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-Apr-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1541  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 30..1541  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-123-427-5  
Alignment Scores:  
Pred. No.: 4.69e-41 Length: 1560  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0  
US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-123-427-5 (1-1560)  
QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20  
DB 1338 CAAAGCCGACCTTAACCTGCACTGCAACCAACGACGACGACGACGACGACGACG 1397  
QY 21 SerAspGlyIleuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40  
DB 1398 TCTGACGAGGCGCTCTCCGCTCCGCGCCGCGCCGCGCCGCTCCGCTCCGCGCGT 1457  
QY 41 ArgValGluProGlyTrpValaPheAlaGluPheTrpArgLeuTrpSerValaAspHisGly 60  
DB 1458 CGGTGAGGCCCTTAATGAGCTTGTGAGTTTACCGCTTGAGGCGGTGACCATGCGC 1517





Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-158-895-42 (1-1568)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20  
DB 1346 CAAGAGCCGAGCCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 1405  
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40  
DB 1406 TCTGACGAGGAGCCTTCCGCTCCCGGCCCCCACTGCTCCGCGCTGGGAGGACGGT 1465  
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60  
DB 1466 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCCTCTGGAGCGTGGACCATGGC 1525  
QY 61 GlnGlnSerValValThrAlaPro 68  
DB 1526 GAGCAGAGCGGTGTGACAGCACCG 1549

## RESULT 6

US-10-384-743-42  
Sequence 42, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIRO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 42  
LENGTH: 1568  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (11)..(1549)  
US-10-384-743-42

## Alignment Scores:

Pred. No.: 4.72e-41  
Score: 359.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 16

Length: 1568  
Matches: 68  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Gaps: 0

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-384-743-42 (1-1568)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20  
DB 1346 CAAGAGCCGAGCCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 1405  
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40  
DB 1406 TCTGACGAGGAGCCTTCCGCTCCCGGCCCCCACTGCTCCGCGCTGGGAGGACGGT 1465  
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60  
DB 1466 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCCTCTGGAGCGTGGACCATGGC 1525

QY 61 GlnGlnSerValValThrAlaPro 68  
DB 1526 GAGCAGAGCGGTGTGACAGCACCG 1549

## RESULT 7

US-10-158-895-10  
Sequence 10, Application US/10158895  
Publication No. US20020155624A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIRO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 1569  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (77)..(1557)  
US-10-158-895-10

## Alignment Scores:

Pred. No.: 4.72e-41  
Score: 359.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 13

Length: 1569  
Matches: 68  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Gaps: 0

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-158-895-10 (1-1569)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20  
DB 1315 CAAGAGCCGAGCCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 1374  
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40  
DB 1375 TCTGACGAGGAGCCTTCCGCTCCCGGCCCCCACTGCTCCGCGCTGGGAGGACGGT 1434  
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60  
DB 1435 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCCTCTGGAGCGTGGACCATGGC 1494  
QY 61 GlnGlnSerValValThrAlaPro 68  
DB 1495 GAGCAGAGCGGTGTGACAGCACCG 1518

## RESULT 8

US-10-384-743-10  
Sequence 10, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIRO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279



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; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3349
; LENGTH: 16877
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-515-3349

```

## Alignment Scores:

```

Pred. No.: 7,95e-40 Length: 16877
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

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US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-242-515-3349 (1-16877)

```

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSer 20
Db 15011 CAAAGCCGACCTTAACCTGACGTCCACCAACGACGACGACGACGACGACGACGACG 15070
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGlyAspGly 40
Db 15071 TCTGACGAGGCGCTCTCCGCTCCGCGCCGCGCCACCTGCTCCGCTGCGAGAGCGT 15130
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60
Db 15131 CGGTGTGAGCCCTATGAGACTTGTGAGTTTACCGCTCTGAGCGTGAACCATGGC 15190
QY 61 GlnGlnSerValValThrAlaPro 68
Db 15191 GAGCAGAGCGTGTGACGACGACG 15214

```

## RESULT 12

```

US-09-925-300-330
; Sequence 330, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 330
; LENGTH: 696
; TYPE: DNA

```

```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (643)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (657)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (685)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-330

```

## Alignment Scores:

```

Pred. No.: 1.81e-40 Length: 696
Score: 352.00 Matches: 67
Percent Similarity: 98.53% Conservative: 0
Best Local Similarity: 98.53% Mismatches: 1
Query Match: 98.05% Indels: 0
DB: 9 Gaps: 0

```

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-09-925-300-330 (1-696)

```

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSer 20
Db 49 CAAAGCCGACCTTAACCTGACGTCCACCAACGACGACGACGACGACGACGACGACG 108
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGlyAspGly 40
Db 109 TCTRACGAGGCGCTCTCCGCTCCGCGCCGCGCCACCTGCTCCGCTGCGAGAGCGT 168
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60
Db 169 CGGTGTGAGCCCTATGAGACTTGTGAGTTTACCGCTCTGAGGCGTGAACCATGGC 228
QY 61 GlnGlnSerValValThrAlaPro 68
Db 229 GAGCAGAGCGTGTGACGACGACG 252

```

## RESULT 13

```

US-09-918-995-32946
; Sequence 32946, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hysq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: FROM VARIOUS CDNA LIBRARIES
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32946
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-32946

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## Alignment Scores:

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Pred. No.: 6.97e-40 Length: 409
Score: 346.00 Matches: 65
Percent Similarity: 97.06% Conservative: 1
Best Local Similarity: 95.59% Mismatches: 2
Query Match: 96.38% Indels: 0
DB: 10 Gaps: 0

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US-09-830-144-4\_COPY\_437\_504 (1-68) x US-09-918-995-32946 (1-409)

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QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSer 20
Db 48 CAAAGCCGACCTTAACCTGACGTCCACCAACGACGACGACGACGACGACGACGACG 107

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**Best Available Copy**